BIOMATH
www.biomathforum.org/biomath/index.php/biomath
Biomath Forum

ORIGINAL ARTICLE

Modeling the Dynamics of Arboviral Diseases with Vaccination Perspective

Hamadjam Abboubakar*, Jean C. Kamgang†, Léontine N. Nkamba‡, Daniel Tieudjo† and Lucas Emini¶
*Department of Computer Science, UIT–University of Ngaoundéré, Cameroon
abboubakarhamadjam@yahoo.fr
†Department of Mathematics and Computer Science, ENSAI–University of Ngaoundéré, Cameroon
jckamgang@yahoo.fr, tieudjo@yahoo.com
‡Department of Mathematics, ENS–University of Yaoundé I,
lnkague@gmail.com
¶Department of Mathematics, Polytechnic–St. Jerome Catholic University, Cameroon
lemini@univ-catho-sjd.com

Received: 31 December 2014, accepted: 24 July 2015, published: 27 August 2015

***Abstract*—In this paper, we propose a model of transmission of arboviruses, which takes into account a future vaccination strategy in human population. A qualitative analysis based on stability and bifurcation theory reveals that the phenomenon of backward bifurcation may occur; the stable disease-free equilibrium of the model coexists with a stable endemic equilibrium when the associated reproduction number, R_0, is less than unity. We show that the backward bifurcation phenomenon is caused by the arbovirus induced mortality. Using the direct Lyapunov method, we prove the global stability of the trivial equilibrium. Through a global sensitivity analysis, we determine the relative importance of model parameters for disease transmission. Simulation results using a nonstandard qualitatively stable numerical scheme are provided to illustrate the impact of vaccination strategy in human communities.**

***Keywords*-Mathematical model; Arboviral disease; Vaccination; Stability; Backward bifurcation; Sensitivity analysis; Nonstandard numerical scheme.**

I. Introduction

Arboviral diseases are affections transmitted by hematophagous arthropods. There are currently 534 viruses registered in the International Catalogue of Arboviruses and 25% of them have caused documented illness in humans [20], [49], [42]. Examples of these kinds of diseases are dengue, yellow fever, Saint Louis fever, encephalitis, West Nile Fever and chikungunya. A wide range of arbovirus diseases are transmitted by mosquito bites and constitute a public health emergency of international concern. According to WHO, dengue, caused by any of four closely-related virus serotypes (DEN-1-4) of the genus Flavivirus, causes 50–100 million infections worldwide every year, and the majority of patients worldwide are children aged 9 to 16 years [72], [84], [86]. The dynamics of arboviral diseases like dengue or chikungunya are influenced by many factors such as humans, the mosquito vector, the virus itself, as well as the environment which affects all the present mechanisms of control directly

Citation: Hamadjam Abboubakar, Jean C. Kamgang, Léontine N. Nkamba, Daniel Tieudjo, Lucas Emini, Modeling the Dynamics of Arboviral Diseases with Vaccination Perspective, Biomath 4 (2015), 1507241, http://dx.doi.org/10.11145/j.biomath.2015.07.241

or indirectly.

For all mentioned diseases, only yellow fever has a licensed vaccine. However, some works are underway for development of a vaccine for dengue [10], [11], [33], [50], [73], [85], Japanese encephalitis [73], and Chikungunya [53], [54], [55], [46]. Moreover, the existence of different strains of dengue virus, for example, makes the developpement of an efficient vaccine a challenge for scientists. However, according to the French newspaper Le Figaro, the SANOFI laboratory hopes to market in the second half of 2015, the first vaccine against dengue fever, with an overall efficacy of 61% vaccine among young people aged 9 to 16 years and the rate of protection against severe dengue 95.5% [39]. Therefore, it is important to assess the potential impact of such vaccines in human communities.

As part of the necessary multi–disciplinary research approach, mathematical models have been extensively used to provide a framework for understanding arboviral diseases transmission and control strategies of the infection spread in the host population. In the literature, considerable works can be found on the mathematical modeling of specific arboviral diseases, like West Nile Fever, yellow fever, dengue and chikungunya, see e.g. [2], [17], [24], [30], [35], [36], [38], [40], [56], [60], [61], [64], [68], [79]. Although these models highlight the means to fight against these arbovirus, few papers deal with models that consider vaccination [40], [68], [79].

In this paper, we formulate a model, described by differential equations, in which we include two aspects: vaccination in the human population and the aquatic stage in the vectors population.We perform a qualitative analysis of the model, based on stability and bifurcation theory. In particular, we use an approach based on the center manifold theory [19], [31], [43] to evaluate the occurrence of a transcritical backward bifurcation and, as a consequence, the presence of multiple endemic equilibria when the basic reproduction number R_0 is less than unity. Under the point of view of disease control, the occurrence of backward bifurcation has relevant implications for disease control because the classical threshold condition $R_0 < 1$, is no longer sufficient to ensure the elimination of the disease from the population.

The global stability of the trivial equilibrium and the disease–free equilibrium (the equilibrium without disease in both populations), whenever the associated thresholds (the net reproductive number $\mathcal{N}$ and the basic reproduction number R_0) are less than unity, is derived through the use of Lyapunov stability theory and LaSalle's invariant set theorem, and the approach of Kamgang and Sallet [48], respectively.

Through global sensitivity analysis, we determine the relative importance of model parameters for disease transmission. The analysis of the model is completed by the construction of a nonstandard numerical scheme which is qualitatively stable.

The rest of this paper is organized as follows. In Section II, we develop the mathematical model and give the invariant set in which the model is defined. In Section III, we compute two thresholds: the net reproductive number $\mathcal{N}$ and the basic reproduction number R_0. Depending of the values of these thresholds, we identify two disease–free equilibria: the trivial equilibrium which corresponds to the extinction of vectors, when $\mathcal{N} \leq 1$, and the disease-free equilibrium (DFE) when $\mathcal{N} > 1$ and $R_0 < 1$. The results concerning the local and global stability of these two equilibria are also given. The section IV is devoted to the existence of endemic equilibria and bifurcation analysis. Vaccine impact is evaluated in Section V. Uncertainty and sensitivity analysis and the construction of a stable numerical scheme, are made in sections VI and VII respectively. A conclusion completes the paper.

II. Model formulation, Invariant region.

In this section we describe the mathematical model that we shall study in this paper. The formulation is mostly inspired, with some exceptions, by the models proposed in [30], [40], [68], [80]. We assume that the human and vector populations

are divided into compartments described by time–dependent state variables. This said, the compartments in which the populations are divided are the following ones:

–For humans, we consider susceptible (denoted by S_h), vaccinated (V_h), exposed (E_h), infectious (I_h) and resistant or immune (R_h). Humans susceptible population is recruited at a constant rates Λ_h. Each human subpopulation comes out from the dynamics at natural mortality rates μ_h. The human susceptible population decreased following infection, which can be acquired via effective contact with an exposed or infectious vector at a rate λ_h (the incidence rate of infection for humans), given by

$$\lambda_h = a\tilde{\beta}_{hv}\frac{N_v}{N_h+m}\frac{(\eta_v E_v + I_v)}{N_v} = \beta_{hv}\frac{(\eta_v E_v + I_v)}{N_h+m}, \tag{1}$$

where m denote the alternatively sources of blood [1], [80], a is the biting rate per susceptible vector, $\tilde{\beta}_{hv}$ denotes the probability of transmission of infection from an infectious vector (E_v or I_v) to a susceptible human (S_h or V_h). We obtain the expression of λ_h as follows: the probability that a vector chooses a particular human or other source of blood to bite can be assumed as $\frac{1}{N_h+m}$. Thus, a human receives in average $a\frac{N_v}{N_h+m}$ bites per unit of times. Then, the infection rate per susceptible human is given $a\tilde{\beta}_{hv}\frac{N_v}{N_h+m}\frac{(\eta_v E_v + I_v)}{N_v}$. In expression (1), the modification parameter $0 < \eta_v < 1$ accounts for the assumed reduction in transmissibility of exposed mosquitoes relative to infectious mosquitoes. It is worth emphasizing that, unlike many of the published modelling studies on dengue transmission dynamics, we assume in this study that exposed vectors can transmit dengue disease to humans. This is in line with some studies (see, for instance [34], [40], [87], [90]). However, it is significant to note that, in the case of Chikungunya for example, the exposed vectors do not play any role in the infectious process, in this case $\eta_v = 0$.

The vaccinated population is generated by vaccination of susceptible humans at a rate ξ. Further, it is expected that any future dengue vaccine would be imperfect [40], [68]. Thus, vaccinated individuals acquire infection at a rate $(1-\epsilon)\lambda_h$ where ϵ is the vaccine efficacy. Exposed humans develop clinical symptoms of disease, and move to the infectious class at rate γ_h. Infectious humans may die as consequence of the infection, at a disease–induced death rate δ, or recover at a rate σ. It is assumed that individuals successfully acquire lifelong immunity against the virus.

–Vectors population is classified into four compartments: susceptible (S_v), exposed (E_v), infectious (I_v) and aquatic (A_v). The aquatic state includes the eggs, larvae, and pupae. The vector population does not have an immune class, since it is assumed that their infectious period ends with their death. The population of vectors consists essentially of females which reached adulthood. A susceptible vector is generated by the adulthood females at rate θ. The susceptible vector population decreased following infection, which can be acquired via effective contact with an exposed or infectious human at a rate λ_v (the incidence rate of infection for vectors), given by

$$\lambda_v = a\tilde{\beta}_{vh}\frac{(\eta_h E_h + I_h)}{N_h}\frac{N_h}{N_h+m} = \beta_{vh}\frac{(\eta_h E_h + I_h)}{N_h+m} \tag{2}$$

where $\tilde{\beta}_{vh}$ is the probability of transmission of infection from an infectious human (E_h or I_h) to a susceptible vector (S_v), where the modification parameter $0 \leq \eta_h < 1$ accounts for the relative infectiousness of exposed humans in relation to infectious humans. Here too, it is assumed that susceptible mosquitoes can acquire infection from exposed humans [23], [40]. Exposed vectors move to the infectious class with the rate γ_v. As in the case of the outbreak of Chikungunya on Réunion Island, it has been shown that lifespan of the infected mosquitoes is almost halved. This particular feature of infected mosquitoes therefore influences the dynamics of the disease [32], [30]. Thus, following Dumont and coworkers [29], [30], we assume in this work that the lifespan of a vector depends on its epidemiological status. So the average lifespan for susceptible mosquitoes is

TABLE I
THE STATE VARIABLES OF MODEL (3).

	Humans		Vectors
S_h:	Susceptible	A_v	Aquatic
V_h:	Vaccined	S_v:	Susceptible
E_h:	Infected	E_v:	Exposed
I_h:	Infectious	I_v:	Infectious
R_h:	Resistant (immune)		

TABLE II
DESCRIPTION OF PARAMETERS OF MODEL (3).

Parameter	Description
Λ_h	Recruitment rate of humans
ξ	Vaccine coverage
ϵ	The vaccine efficacy
η_h, η_v	Modification parameters
$\tilde{\beta}_{hv}$	Probability of transmission of infection from an infectious vector to a susceptible human
$\tilde{\beta}_{vh}$	Probability of transmission of infection from an infectious humans to a susceptible vector
γ_h	Progression rate from E_h to I_h
γ_v	Progression rate from E_v to I_v
μ_h	Natural mortality rate in humans
μ_v	Natural mortality rate of susceptible vectors
μ_A	Natural mortality of larvae
μ_1^{-1}	Average lifespan of exposed mosquitoes
μ_2^{-1}	Average lifespan of infected mosquitoes
θ	Maturation rate from larvae to adult
δ	Disease–induced death rate in humans
σ	Recovery rate for humans
a	Average number of bites
m	Number of alternative source of blood
K	Capacity of breeding sites
μ_b	Number of eggs at each deposit per capita

$1/\mu_v$ days, the average lifespan of the exposed mosquitoes is $1/\mu_1$ days and the average adult lifespan for infected vector is $1/\mu_2$. Thus, we have $1/\mu_2 \leq 1/\mu_1 \leq 1/\mu_v$ (with equality for other arboviral diseases). We do not consider vertical transmission in this work, so only susceptible humans are recruited, and vectors are assumed to be born susceptible.

We are now in position to write the model (the meaning of the state variables and parameters are summarized in Table I and Table II:

$$\begin{cases} \dot{S}_h &= \Lambda_h - \lambda_h S_h - \xi S_h - \mu_h S_h \\ \dot{V}_h &= \xi S_h - (1-\epsilon)\lambda_h V_h - \mu_h V_h \\ \dot{E}_h &= \lambda_h \left[S_h + (1-\epsilon)V_h\right] - (\mu_h + \gamma_h)E_h \\ \dot{I}_h &= \gamma_h E_h - (\mu_h + \delta + \sigma)I_h \\ \dot{R}_h &= \sigma I_h - \mu_h R_h \\ \dot{A}_v &= \mu_b \left(1 - \dfrac{A_v}{K}\right)(S_v + E_v + I_v) - (\theta + \mu_A)A_v \\ \dot{S}_v &= \theta A_v - \lambda_v S_v - \mu_v S_v \\ \dot{E}_v &= \lambda_v S_v - (\mu_1 + \gamma_v)E_v \\ \dot{I}_v &= \gamma_v E_v - \mu_2 I_v \end{cases} \tag{3}$$

In model (3) the upper dot denotes the time derivative. K denote the carrying capacity of breeding sites. The parameter K is highly dependent on some factors such as (the location, temperature, season). In this work, we follow Dumont and Chiroleu [30], and consider, in our sensitive analysis, that K depend of the location, thus $K = \chi N_h$, where χ is a positive integer which represent the location and N_h the human population size. For example, in the year 2005 at Saint-Denis and Saint-Pierre in Réunion island, $\chi = 2$) [30]. μ_b represent the number of eggs at each deposit per capita and μ_A is the natural mortality of larvae.

We set $\pi = 1 - \epsilon$, $k_1 = \mu_h + \xi$, $k_2 = \mu_h + \gamma_h$, $k_3 = \mu_h + \delta + \sigma$, $k_4 = \mu_1 + \gamma_v$, $k_6 = \mu_A + \theta$.

Let N_h the total human population and N_v the total of adult vectors, i.e. $N_h = S_h + V_h + E_h + I_h + R_h$ and $N_v = S_v + E_v + I_v$. System (3) can be rewritten in the following way

$$\frac{dX}{dt} = \mathbb{A}(X)X + F \tag{4}$$

with $X = (S_h, V_h, E_h, I_h, R_h, A_v, S_v, E_v, I_v)^T$, $\mathbb{A}(X) = (\mathbb{A}_{ij})_{1\leq i,j\leq 9}$ were $\mathbb{A}_{1,1} = -(\lambda_h + k_1)$, $\mathbb{A}_{2,1} = \xi$, $\mathbb{A}_{2,2} = -(\pi\lambda_h + \mu_h)$, $\mathbb{A}_{3,1} = \lambda_h$, $\mathbb{A}_{3,2} = \pi\lambda_h$, $\mathbb{A}_{3,3} = -k_2$, $\mathbb{A}_{4,3} = \gamma_h$, $\mathbb{A}_{4,4} = -k_3$, $\mathbb{A}_{5,4} = \sigma$, $\mathbb{A}_{5,5} = -\mu_h$, $\mathbb{A}_{6,7} = \mathbb{A}_{6,8} = \mathbb{A}_{6,9} = \mu_b$, $\mathbb{A}_{7,6} = \theta$, $\mathbb{A}_{7,7} = -(\lambda_v + \mu_v)$, $\mathbb{A}_{8,7} = \lambda_v$, $\mathbb{A}_{8,8} = -k_4$, $\mathbb{A}_{9,8} = \gamma_v$, $\mathbb{A}_{9,9} = -\mu_2$, $\mathbb{A}_{6,6} = -\left(k_6 + \mu_b \dfrac{S_v + E_v + I_v}{K}\right)$ and the other entries of $\mathbb{A}(X)$ are equal to zero; and $F = (\Lambda_h, 0, 0, 0, 0, 0, 0, 0, 0)^T$.

Note that $\mathbb{A}(X)$ is a Metzler matrix, i.e. a matrix such that off diagonal terms are non negative [8], [47], for all $X \in \mathbf{R}^9_+$. Thus, using the fact that $F \geq 0$, system (4) is positively invariant in $\mathbf{R}^9_+$,

which means that any trajectory of the system starting from an initial state in the positive orthant $\mathbf{R}^9_+$, remains forever in $\mathbf{R}^9_+$. The right-hand side is Lipschitz continuous: there exists an unique maximal solution.

On the other hand, from the first four equations of model system (3), it follows that

$$\dot{N}_h(t) = \Lambda_h - \mu_h N_h - \delta I_h \leq \Lambda_h - \mu_h N_h. \quad (5)$$

So that

$$0 \leq N_h(t) \leq \frac{\Lambda_h}{\mu_h} + \left(N_h(0) - \frac{\Lambda_h}{\mu_h}\right) e^{-\mu_h t}. \quad (6)$$

Thus, at $t \longrightarrow \infty$, $0 \leq N_h(t) \leq \dfrac{\Lambda_h}{\mu_h}$.

From the last three equations of model system (3), it also follows that

$$\begin{aligned} \dot{N}_v(t) &= \theta A_v - \mu_v S_v - \mu_1 E_v - \mu_2 I_v \\ &\leq \theta A_v - \mu_v N_v. \end{aligned} \quad (7)$$

So that

$$0 \leq N_v(t) \leq \frac{\theta A_v}{\mu_v} + \left(N_v(0) - \frac{\theta A_v}{\mu_v}\right) e^{-\mu_v t}. \quad (8)$$

Thus, at $t \longrightarrow \infty$, $0 \leq N_v(t) \leq \dfrac{\theta K}{\mu_v}$ since $A_v \leq K$. Therefore, all feasible solutions of model system (3) enter the region:

$$\begin{aligned} \mathcal{D} = \big\{ &(S_h, V_h, E_h, I_h, R_h, A_v, S_v, E_v, I_v) \in \mathbf{R}^9 : \\ &S_h + V_h + E_h + I_h + R_h \leq \frac{\Lambda_h}{\mu_h}; A_v \leq K; \\ &S_v + E_v + I_v \leq \theta K/\mu_v \big\}. \end{aligned}$$

III. The disease–free equilibria and stability analysis

Now let $\mathcal{N}$ the net reproductive number [25] given by

$$\mathcal{N} = \frac{\mu_b \theta}{\mu_v(\theta + \mu_A)}. \quad (9)$$

We prove the following result

Proposition 3.1: a) If $\mathcal{N} \leq 1$, then, system (3) has only one trivial disease–free equilibrium $TE := P_0 = \left(\dfrac{\Lambda_h}{k_1}, \dfrac{\xi\Lambda_h}{\mu_h k_1}, 0, 0, 0, 0, 0, 0, 0\right)$.
b) If $\mathcal{N} > 1$, then, system (3) has a Disease–Free Equilibrium $P_1 = \left(S_h^0, V_h^0, 0, 0, 0, A_v^0, S_v^0, 0, 0\right)$, with

$$S_h^0 = \frac{\Lambda_h}{k_1},\ V_h^0 = \frac{\xi\Lambda_h}{k_1\mu_h},\ A_v^0 = K\left(1 - \frac{1}{\mathcal{N}}\right),$$
$$S_v^0 = \frac{\theta}{\mu_v} K\left(1 - \frac{1}{\mathcal{N}}\right).$$

Proof: See Appendix A. ■

In Proposition 3.1, we have shown that system (3) have at least two equilibria depending of the value of treshold $\mathcal{N}$ and the basic reproduction number R_0. Precisely, we have proved that when $\mathcal{N} \leq 1$, model sytem (3) admits only one equilibrium called trivial equilibrium ($TE := P_0$). When $\mathcal{N} > 1$, model sytem (3) admits additionally the disease–free equilibrium ($DFE := P_1$). We prove, in the following, that the trivial equilibrium is locally and globally asymptotically stable whenever $\mathcal{N} \leq 1$. Then, we prove that the trivial equilibrium is unstable when $\mathcal{N} > 1$, and the disease–free equilibrium is locally asymptotically stable whenever $R_0 < 1$. Using Kamgang and Sallet approach [48], a necessary condition for the global stabilty of the disease–free equilibrium is also given.

A. Local stability analysis

The local stability of the trivial equilibrium and the disease–free equilibrium is given in the following result:

Proposition 3.2: a) If $\mathcal{N} \leq 1$, then the trivial equilibrium TE is locally asymptotically stable.
b) If $\mathcal{N} > 1$, then the trivial equilibrium is unstable and the Disease Free Equilibrium P_1 is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$, where R_0 is the basic reproduction number [26], [82], given by

$$\begin{aligned} R_0^2 = &\frac{\beta_{hv}\beta_{vh} K\theta(\pi\xi + \mu_h)(k_3\eta_h + \gamma_h)}{(\mu_h + \xi)(\mu_h + \gamma_h)(\mu_h + \delta + \sigma)} \\ &\times \frac{\Lambda_h\mu_h(\mu_2\eta_v + \gamma_v)}{\mu_v\mu_2(\Lambda_h + m\mu_h)^2(\mu_1 + \gamma_v)} \left(1 - \frac{1}{\mathcal{N}}\right). \end{aligned} \quad (10)$$

Proof: See appendix B. ■

B. Global stability analysis

1) Global asymptotic stability of the trivial equilibrium $TE := P_0$:

Proposition 3.3: If $\mathcal{N} \leq 1$, then, $TE := P_0$ is globally asymptotically stable on $\mathcal{D}$.

Proof: See Appendix C. ■

2) Global asymptotic stability of the disease–free equilibrium : Following [30], we prove that the disease–free equilibrium $DFE := P_1$ is globally asymptotically stable under a certain threshold condition. To this aim, we use a result obtained by Kamgang and Sallet [48], which is an extension of some results given in [82]. Using the property of DFE, it is possible to rewrite (3) in the following manner

$$\begin{cases} \dot{X}_S = & \mathcal{A}_1(X)(X_S - X_{DFE}) + \mathcal{A}_{12}(X)X_I \\ \dot{X}_I = & \mathcal{A}_2(X)X_I \end{cases} \tag{11}$$

where X_S is the vector representing the state of different compartments of non transmitting individuals (S_h, V_h, R_h, A_v, S_v) and the vector X_I represents the state of compartments of different transmitting individuals (E_h, I_h, E_v, I_v). Here, we have $X_S = (S_h, V_h, R_h, A_v, S_v)^T$, $X_I = (E_h, I_h, E_v, I_v)^T$, $X = (X_S, X_I)$ and $X_{DFE} = \left(S_h^0, V_h^0, 0, 0, 0, A_v^0, S_v^0, 0, 0\right)^T$, with

$$\mathcal{A}_1(X) = \begin{pmatrix} -k_1 & 0 & 0 & 0 & 0 \\ \xi & -\mu_h & 0 & 0 & 0 \\ 0 & 0 & -\mu_h & 0 & 0 \\ 0 & 0 & 0 & -K_6 & K_7 \\ 0 & 0 & 0 & \theta & -\mu_v \end{pmatrix},$$

$$\mathcal{A}_{12}(X) = \begin{pmatrix} 0 & 0 & -a_{13} & -a_{14} & 0 \\ 0 & 0 & -a_{23} & -a_{24} & 0 \\ 0 & \sigma & 0 & 0 & 0 \\ 0 & 0 & \kappa & \kappa & 0 \\ -a_{41} & -a_{42} & 0 & 0 & 0 \end{pmatrix},$$

$$\mathcal{A}_2(X) = \begin{pmatrix} -k_2 & 0 & b_{13} & b_{14} \\ \gamma_h & -k_3 & 0 & 0 \\ b_{31} & b_{32} & -k_4 & 0 \\ 0 & 0 & \gamma_v & -\mu_2 \end{pmatrix},$$

with $K_6 = \left(k_6 + \mu_b \frac{S_v^0}{K}\right)$, $K_7 = \mu_b\left(1 - \frac{A_v}{K}\right)$, $a_{13} = \frac{\beta_{hv}\eta_v S_h}{N_h + m}$, $a_{14} = \frac{\beta_{hv} S_h}{N_h + m}$, $a_{23} = \frac{\pi\beta_{hv}\eta_v V_h}{N_h + m}$, $a_{24} = \frac{\pi\beta_{hv} V_h}{N_h + m}$, $a_{41} = \frac{\beta_{vh}\eta_h S_v}{N_h + m}$, $a_{42} = \frac{\beta_{vh} S_v}{N_h + m}$, $b_{13} = \frac{\beta_{hv}\eta_v H}{N_h + m}$, $b_{14} = \frac{\beta_{hv} H}{N_h + m}$, $b_{31} = \frac{\beta_{vh}\eta_h S_v}{N_h + m}$, $b_{32} = \frac{\beta_{vh} S_v}{N_h + m}$, $\kappa = \mu_b\left(1 - \frac{A_v}{K}\right)$ and $H = (S_h + \pi V_h)$.

A direct computation shows that the eigenvalues of $\mathcal{A}_1(X)$ are real and negative. Thus the system $\dot{X}_S = \mathcal{A}_1(X)(X_S - X_{DFE})$ is globally asymptotically stable at X_{DFE}. Note also that $\mathcal{A}_2(X)$ is a Metzler matrix, i.e. a matrix such that off diagonal terms are non negative [8], [47].

Following $\mathcal{D}$, we now consider the bounded set $\mathcal{G}$:

$$\begin{aligned} \mathcal{G} = \big\{ & (S_h, V_h, E_h, I_h, R_h, A_v, S_v, E_v, I_v) \in \mathbf{R}^9 : \\ & S_h \leq N_h, V_n \leq N_h, E_h \leq N_h, I_h \leq N_h, R_h \leq N_h, \\ & \bar{N_h} = \Lambda_h/(\mu_h + \delta) \leq N_h \leq N_h^0 = \Lambda_h/\mu_h; \\ & A_v \leq K; S_v + E_v + I_v \leq \theta K/\mu_v \big\}. \end{aligned}$$

Let us recall the following theorem [48]

Theorem 3.1: Let $\mathcal{G} \subset \mathcal{U} = \mathbf{R}^5 \times \mathbf{R}^4$. The system (11) is of class C^1, defined on $\mathcal{U}$. If

(1) $\mathcal{G}$ is positively invariant relative to (11).
(2) The system $\dot{X}_S = \mathcal{A}_1(X)(X_S - X_{DFE})$ is Globally asymptotically stable at X_{BRDFE}.
(3) For any $x \in \mathcal{G}$, the matrix $\mathcal{A}_2(X)$ is Metzler irreducible.
(4) There exists a matrix $\bar{\mathcal{A}}_2$, which is an upper bound of the set $\mathcal{M} = \{\mathcal{A}_2(x) \in \mathcal{M}_4(\mathbf{R}) : x \in \mathcal{G}\}$ with the property that if $\mathcal{A}_2 \in \mathcal{M}$, for any $\bar{x} \in \mathcal{G}$, such that $\mathcal{A}_2(\bar{x}) = \bar{\mathcal{A}}_2$, then $\bar{x} \in \mathbf{R}^5 \times \{0\}$.
(5) The stability modulus of $\bar{\mathcal{A}}_2$, $\alpha(\mathcal{A}_2) = \max_{\lambda \in sp(\mathcal{A}_2)} \mathcal{R}\mathbf{e}(\lambda)$ satisfied $\alpha(\mathcal{A}_2) \leq 0$.

Then the DFE is GAS in $\mathcal{G}$. (See [48] for a proof).

Let us now verify the assumptions of the previous theorem: it is obvious that conditions (1–3) of the theorem are satisfied. An upper bound of the set of matrices $\mathcal{M}$, which is the matrix $\bar{\mathcal{A}}_2$ is given

by

$$\bar{\mathcal{A}}_2 = \begin{pmatrix} -k_2 & 0 & \bar{b}_{13} & \bar{b}_{14} \\ \gamma_h & -k_3 & 0 & 0 \\ \dfrac{\beta_{vh}\eta_h \bar{S}_v}{\bar{N}_h + m} & \dfrac{\beta_{vh}\bar{S}_v}{\bar{N}_h + m} & -k_4 & 0 \\ 0 & 0 & \gamma_v & -\mu_2 \end{pmatrix},$$

where $\bar{b}_{13} = \dfrac{\beta_{hv}\eta_v(\bar{S}_h + \pi\bar{V}_h)}{\bar{N}_h + m}$, $\bar{b}_{14} = \dfrac{\beta_{hv}(\bar{S}_h + \pi\bar{V}_h)}{\bar{N}_h + m}$, $\bar{S}_h = S_h^0$, $\bar{V}_h = V_h^0$, $\bar{A}_v = K$, $\bar{S}_v = \dfrac{\theta}{\mu_v}K$, and $\bar{N}_h = \dfrac{\Lambda_h}{(\mu_h + \delta)}$.

To check condition (5) in theorem 3.1, we will use the following useful lemma [48] which is the a characterization of Metzler stable matrices:

Lemma 3.1: Let M be a square Metzler matrix written in block form $\begin{pmatrix} A & B \\ C & D \end{pmatrix}$ with A and D square matrices. M is Metzler stable if and only if matrices A and
$D - CA^{-1}B$ are Metzler stable.

A necessary condition for a Metzler matrix to be stable is that the elements on the diagonal are negative. Note also that A is a Metzler stable matrix is equivalent to A is invertible and $-A^{-1} \geq 0$. Lemma 3.1 allows to reduce the problem of Metzler stability, by induction, to the stability of 2×2 Metzler matrices [48]. In our case, we have
$A = \begin{pmatrix} -k_2 & 0 \\ \gamma_h & -k_3 \end{pmatrix}$,
$B = \begin{pmatrix} \dfrac{\beta_{hv}\eta_v(\bar{S}_h + \pi\bar{V}_h)}{\bar{N}_h + m} & \dfrac{\beta_{hv}(\bar{S}_h + \pi\bar{V}_h)}{\bar{N}_h + m} \\ 0 & 0 \end{pmatrix}$,
$C = \begin{pmatrix} \dfrac{\beta_{vh}\eta_h\bar{S}_v}{\bar{N}_h + m} & \dfrac{\beta_{vh}\bar{S}_v}{\bar{N}_h + m} \\ 0 & 0 \end{pmatrix}$, and
$D = \begin{pmatrix} -k_4 & 0 \\ \gamma_v & -\mu_2 \end{pmatrix}$.

Clearly, A is a stable Metzler matrix. Then, after some computations, we obtain $D - CA^{-1}B$ is a stable Metzler matrix if and only if

$$R_G^2 \leq 1 \tag{12}$$

where

$$R_G^2 = \frac{\beta_{hv}\beta_{vh}K\theta\Lambda_h(\eta_v\mu_2 + \gamma_v)(k_3\eta_h + \gamma_h)}{\mu_v\mu_2\mu_h k_1 k_2 k_3 k_4} \times \frac{(\mu_h + \pi\xi)(\mu_h + \delta)^2}{(\Lambda_h + m(\mu_h + \delta))^2}$$

Thus we claim the following result

Theorem 3.2: If $\mathcal{N} > 1$ and $R_G^2 \leq 1$, then the disease–free equilibrium P_1 is globally asymptotically stable in $\mathcal{G}$.

Remark 3.1: Note that

$$R_G^2 = R_0^2 \frac{(\mu_h + \delta)^2(\Lambda_h + m\mu_h)^2}{\mu_h^2(\Lambda_h + m(\mu_h + \delta))^2}\left(\frac{\mathcal{N}}{\mathcal{N} - 1}\right)$$

and condition (12) is equivalent to

$$R_0^2 \leq \left(\frac{\mathcal{N} - 1}{\mathcal{N}}\right)\frac{\mu_h^2}{(\mu_h + \delta)^2}\frac{(\Lambda_h + m(\mu_h + \delta))^2}{(\Lambda_h + m\mu_h)^2} \tag{13}$$

In absence of disease–induced death in human ($\delta = 0$), inequality (13) becomes

$$R_0^2 \leq \left(\frac{\mathcal{N} - 1}{\mathcal{N}}\right) < 1. \tag{14}$$

This shows that with the establishment of an effective treatment, it is possible to have R_0 and R_G less than 1.

Theorem (3.2) means that for $R_0 < R_G < 1$, the DFE is the unique equilibrium (no co-existence with an endemic equilibrium). If $R_0 \in [R_G, 1]$, then it is possible to have co-existence with endemic equilibrium. To confirm whether or not the backward bifurcation phenomenon occurs in this case, one could use the approach developed in [19], [31], [82], which is based on the general center manifold theory [43].

IV. The endemic equilibria and bifurcation analysis

A. Existence of endemic equilibria

We now turn to study the existence of an endemic equilibrium of model system (3). Let R_0 the basic reproduction number [26], [82] given by Eq. (10).

we claim the following

Proposition 4.1: Let $\mathcal{N} > 1$ and $\mu_v \leq \mu_1 \leq \mu_2$. Then

(i) There exists at least one endemic equilibrium whenever $R_0 > 1$.
(ii) The backward bifurcation phenomenon may occurs when $R_0 \leq 1$.
(iii) The disease–induced death is responsible of the backward bifurcation phenomenon.
(iv) In the absence of the disease–induced death ($\delta = 0$ and $\mu_v = \mu_1 = \mu_2$), system (4) have a unique endemic equilibrium whenever $R_0 > 1$, and the backward bifurcation phenomenon not occurs whenever $R_0 \leq 1$ (See remark 4.1).

Proof: See appendix D. ■

The backward bifurcation phenomenon, in epidemiological systems, indicate the possibility of existence of at least one endemic equilibrium when R_0 is less than unity. Thus, the classical requirement of $R_0 < 1$ is, although necessary, no longer sufficient for disease elimination [6], [14], [40], [75]. In some epidemiological models, it has been shown that the phenomenon of backward bifurcation is caused by factors such as nonlinear incidence (the infection force), disease–induced death or imperfect vaccine [15], [16], [31], [40], [70], [75].

It is important to note that case (i) of Proposition 4.1 suggests the possibility of a pithcfork (Forward) bifurcation when $R_0 = 1$. Also, case (iv) of Proposition 4.1 suggests that the principal cause of occurence of backward bifurcation phenomenon is the disease-induced death in both humans and vectors.

In the following remark, we prove that, in absence of disease–induced death in both populations, the disease–free equilibrium is the unique equilibrium whenever $\mathcal{N} > 1$ and $R_0|_{\delta=0,\mu_v=\mu_1=\mu_2} < 1$. Using the direct Lyapunov method, we prove the global asymptotic stability of the disease–free equilibrium whenever $R_0|_{\delta=0,\mu_v=\mu_1=\mu_2} < 1$.

Remark 4.1: Assumed that $\mathcal{N} > 1$.
Let $k_7 = \Lambda_h + m\mu_h$, $k_8 = \pi\xi + \mu_h$, $k_{11} = k_3\eta_h + \gamma_h$ and $\mathcal{R}_1 = R_0|_{\delta=0,\mu_v=\mu_1=\mu_2}$. In the absence of disease-induced death, i.e, $\delta = 0$ and $\mu_v = \mu_1 = \mu_2$, Eq. (44) (see appendix D) becomes

$$\lambda_h^* \left[B_{02}(\lambda_h^*)^2 + B_{01}\lambda_h^* + B_{00}\right] = 0 \qquad (15)$$

with $B_{02} = k_2k_3k_7^2\pi\mu_v + \beta_{vh}k_7k_{11}\Lambda_h\mu_h\pi > 0$, $B_{00} = k_1k_2k_3k_7^2\mu_h\mu_v\left(1 - \mathcal{R}_1^2\right)$ and $B_{01} = k_1k_2k_3k_7^2\mu_v\pi\left(1 - \mu_h\mathcal{R}_1^2\right) + k_2k_3k_7^2\mu_h\mu_v + \beta_{vh}k_7k_8k_{11}\Lambda_h\mu_h$.

Equation (15) have only one positive solution whenever $\mathcal{R}_1 > 1$. If $\mathcal{R}_1 \leq 1$, then coefficients B_{00}, B_{01}, B_{02} are always positive, and the disease-free equilibrium is the unique equilibrium. From this we conclude that the disease–induced mortality is the possible cause for the occurrence of multiple endemic equilibria below the classical threshold $\mathcal{R}_1 = 1$.

The global stability of the disease–free equilibrium may be achieved by Lyapunov method. To this aim, let us consider the following Lyapunov function [37], [40]

$\mathcal{Y} = \sum_{i=1}^{4} g_iI_i$ where $I = (E_h, I_h, E_v, I_v)$ and g_i, $i = 1, \ldots, 4$ are positive weights given by $g_1 = 1$; $g_2 = \dfrac{k_2}{(k_3\eta_h + \gamma_h)}$, $g_3 = \dfrac{k_2k_3(N_h^0 + m)}{\beta_{vh}S_v^0(k_3\eta_h + \gamma_h)}$, $g_4 = \dfrac{\beta_{hv}\left[S_h^0 + \pi V_h^0\right]}{\mu_2(N_h^0 + m)}$.

Along the solutions of (3) we have:

$$\begin{aligned}
\dot{\mathcal{Y}} &= \sum_{i=1}^{4} g_i\dot{I}_i = g_1\dot{E}_h + g_2\dot{I}_h + g_3\dot{E}_v + g_4\dot{I}_v \\
&= g_1\left[\lambda_h\left[S_h + (1-\epsilon)V_h\right] - (\mu_h + \gamma_h)E_h\right] \\
&+ g_2\left[\gamma_hE_h - (\mu_h + \delta + \sigma)I_h\right] \\
&+ g_3\left[\lambda_vS_v - (\mu_1 + \gamma_v)E_v\right] + g_4\left(\gamma_vE_v - \mu_2I_v\right) \\
&= \left(g_1\frac{\beta_{hv}\eta_v\left[S_h + \pi V_h\right]}{N_h^0 + m} + g_4\gamma_v - g_3k_4\right)E_v \\
&+ \left(g_1\frac{\beta_{hv}\left[S_h + \pi V_h\right]}{N_h^0 + m} - g_4\mu_2\right)I_v \\
&+ \left(g_3\frac{\beta_{vh}\eta_hS_v}{N_h^0 + m} + g_2\gamma_h - g_1k_2\right)E_h \\
&+ \left(g_3\frac{\beta_{vh}S_v}{N_h^0 + m} - g_2k_3\right)I_h
\end{aligned}$$

After replacing the constants g_i, $i = 1, \ldots, 4$ by their value, and using the fact that $S_h \leq S_h^0$, $V_h \leq V_h^0$, $A_v \leq A_v^0$, and $S_v \leq S_v^0$ in

$$\begin{aligned}
\mathcal{D}_1 &= \{(S_h, V_h, E_h, I_h, R_h, A_v, S_v, E_v, I_v) \in \mathcal{D} : \\
&\quad S_h \leq S_h^0, V_h \leq V_h^0, A_v \leq A_v^0, S_v \leq S_v^0\},
\end{aligned}$$

it follows that

$$\dot{\mathcal{Y}} \leq \left(g_1 \frac{\beta_{hv}\eta_v \left[S_h^0 + \pi V_h^0\right]}{N_h^0 + m} + g_4\gamma_v - g_3 k_4 \right) E_v = \frac{k_2 k_3 k_4 (N_h^0 + m)}{\beta_{vh} S_v^0 (k_3\eta_h + \gamma_h)} \left(\mathcal{R}_1^2 - 1\right) E_v$$

We have $\dot{\mathcal{Y}} \leq 0$ if $\mathcal{R}_1 \leq 1$, with $\dot{\mathcal{Y}} = 0$ if $\mathcal{R}_1 = 1$ or $E_v = 0$. Whenever $E_v = 0$, we also have $E_h = 0$, $I_h = 0$ and $I_v = 0$. Substituting $E_h = I_h = E_v = I_v = 0$ in the first, second, fifth, sixth and seventh equations of Eq. (3) with $\delta_1 = 0$ gives $S_h(t) \to S_h^0$, $V_h(t) \to V_h^0$, $R_h(t) \to 0$, $A_v(t) \to A_v^0$, $S_v(t) \to S_v^0$ as $t \to \infty$. Thus

$$[S_h(t), V_h(t), E_h(t), I_h(t), R_h(t), A_v(t), S_v(t), E_v(t), I_v(t)] \to (S_h^0, V_h^0, 0, 0, 0, A_v^0, S_v^0, 0, 0) \ \ as \ \ t \to \infty.$$

It follows from the LaSalle's invariance principle [45] that every solution of (3) (when $\mathcal{R}_1 \leq 1$), with initial conditions in $\mathcal{D}_1$ converges to P_1, as $t \to \infty$. Hence, the DFE (P_1), of model (3), is GAS in $\mathcal{D}_1$ if $\mathcal{R}_1 \leq 1$.

B. Bifurcation analysis

Previous Analysis state that multiple endemic equilibria may occur althougt $R_0 < 1$. In order to better investigate the variation of model's prediction as R_0 varied, we perform a bifurcation analysis at the criticality, i. e. at the Disease–free Equilibrium $DFE := P_1$ and $R_0 = 1$. On one hand, this will provide a rigorous proof that the occurrence of multiple endemic equilibria comes from a backward bifurcation. On the other hand, we will get also information on the stability of equilibria near the criticality. In particular, on the stability of the endemic equilibrium points emerging from the criticality. We study the center manifold near the criticality by using the approach developed in [19], [31], [82], which is based on the general centre manifold theory [43]. In summary, this approach establishes that the normal form representing the dynamics of the system on the center manifold is given by $\dot{u} = a^\star u^2 + b^\star \varpi u$, where, u represent a real function of real variable,

$$a^\star = \frac{\mathbf{v}}{2} \cdot D_{\mathbf{xx}}\mathbf{f}(\mathbf{x}_0, \varpi)\mathbf{w}^2 \equiv \equiv \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k(0,0)}{\partial x_i \partial x_j} \tag{16}$$

and

$$b^\star = \mathbf{v} \cdot D_{\mathbf{x}\varpi}\mathbf{f}(\mathbf{x}_0, \varpi)\mathbf{w} \equiv \sum_{k,i=1}^{n} v_k w_i \frac{\partial^2 f_k(0,0)}{\partial x_i \partial \varpi}. \tag{17}$$

Note that the symbol ϖ denotes a bifurcation parameter to be chosen, f_i's denotes the right hand side of system (3), $\mathbf{x}$ denotes the state vector, $\mathbf{x}_0$ the Disease–free Equilibrium P_1; $\mathbf{v}$ and $\mathbf{w}$ denote the left and right eigenvectors, respectively, corresponding to the null eigenvalue of the Jacobian matrix of system (3) evaluated at the criticality.

In order to apply this approach, let us choose β_{hv} as bifurcation parameter. From $R_0 = 1$ we get the critical value

$$\beta_{hv}^* = \frac{\mu_v \mu_2 k_1 k_2 k_3 k_4 (\Lambda_h + m\mu_h)^2 \left(\frac{\mathcal{N}}{\mathcal{N}-1}\right)}{\beta_{vh}\Lambda_h\mu_h K\theta(\pi\xi + \mu_h)(\mu_2\eta_v + \gamma_v)\left[\eta_h k_3 + \gamma_h\right])}.$$

Note also that in $f_k(0,0)$, the first zero corresponds to the disease–free equilibrium, P_1, for the system (3). Since $\beta_{hv} = \beta_{hv}^*$ is the bifurcation parameter, it follows from $\varpi = \beta_{hv} - \beta_{hv}^*$ that $\varpi = 0$ when $\beta_{hv} = \beta_{hv}^*$ which is the second component in $f_k(0,0)$.

The Jacobian matrix of the system (4) evaluated at the disease–free equilibrium P_1 with $\beta_{hv} = \beta_{hv}^*$ is given by

$$J(P_1) = \begin{pmatrix} -k_1 & 0 & 0 & 0 & 0 \\ \xi & -\mu_h & 0 & 0 & 0 \\ 0 & 0 & -k_2 & 0 & 0 \\ 0 & 0 & \gamma_h & -k_3 & 0 \\ 0 & 0 & 0 & \sigma & -\mu_h \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -\frac{\beta_{vh}\eta_h S_v^0}{H} & -\frac{\beta_{vh} S_v^0}{H} & \\ 0 & 0 & \frac{\beta_{vh}\eta_h S_v^0}{H} & \frac{\beta_{vh} S_v^0}{H} & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$\begin{pmatrix} 0 & 0 & -\frac{\beta^*_{hv}\eta_v S^0_h}{H} & -\frac{\beta^*_{hv} S^0_h}{H} \\ 0 & 0 & -\frac{\beta^*_{hv}\pi\eta_v V^0_h}{H} & -\frac{\beta^*_{hv}\pi V^0_h}{H} \\ 0 & 0 & \frac{\beta^*_{hv}\eta_v S_0}{H} & \frac{\beta^*_{hv} S_0}{H} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ -K_1 & K_2 & K_2 & K_2 \\ \theta & -\mu_v & 0 & 0 \\ 0 & 0 & -k_4 & 0 \\ 0 & 0 & \gamma_v & -\mu_2 \end{pmatrix},$$

where we have set $H = N^0_h + m$, $K_1 = \dfrac{\mu_b\theta}{\mu_v}$ and $K_2 = \dfrac{k_6\mu_v}{\theta}$.

The eigenvalues of the Jacobian matrix $J(P_1)$ are $\lambda_1 = -\mu_h$, $\lambda_2 = -k_1$, and the other eigenvalues are the eigenvalue of the following matrix

$$\bar{J} = \begin{pmatrix} -k_2 & 0 & 0 & 0 & \frac{\beta^*_{hv}\eta_v S_0}{H} & \frac{\beta^*_{hv} S_0}{H} \\ \gamma_h & -k_3 & 0 & 0 & 0 & 0 \\ 0 & 0 & -K_1 & K_2 & K_2 & K_2 \\ -\frac{\beta_{vh}\eta_h S^0_v}{H} & -\frac{\beta_{vh} S^0_v}{H} & \theta & -\mu_v & 0 & 0 \\ \frac{\beta_{vh}\eta_h S^0_v}{H} & \frac{\beta_{vh} S^0_v}{H} & 0 & 0 & -k_4 & 0 \\ 0 & 0 & 0 & 0 & \gamma_v & -\mu_2 \end{pmatrix}.$$

The characteristic polynomial of $\bar{J}$ is given by

$$f(\lambda) = \lambda^6 + a_5\lambda^5 + a_4\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 \tag{18}$$

with

$$a_0 = -\frac{k_1k_2k_3k_4k_7^2\mu_2\mu_b\mu_v(k_6\mu_v - \mu_b\theta)}{k_1k_7^2\mu_b\mu_v}\left(1 - R_0^2\right).$$

The others coefficients a_5, a_4, a_3, a_2, and a_1 are obtained after computations on Maxima software [58], [89]. Since at the criticality, we have $R_0 = 1$, then $a_0 = 0$, thus equation (18) becomes

$f(\lambda) = \lambda\left(\lambda^5 + a_5\lambda^4 + a_4\lambda^3 + a_3\lambda^2 + a_2\lambda + a_1\right)$. Then, the Jacobian $J(P_1)$ of the linearized system has a simple zero eigenvalue and therefore P_1 is a nonhyperbolic equilibrium for $R_0 = 1$. In order to get the coefficients (16) and (17), we need to calculate the right and the left eigenvectors corresponding to the zero eigenvalue.

The right eigenvector of $J(P_1)$ is given by $\mathbf{w} = (w_1, w_2, w_3, w_4, w_5, w_6, w_7, w_8, w_9)^T$ where

$$w_1 = -\frac{\beta^*_{hv}k_9\mu_h\Lambda_h}{k_1^2\gamma_v k_7}w_9 < 0,$$

$$w_2 = -\frac{\xi\Lambda_h\beta^*_{hv}k_9(\mu_h + k_1\pi)}{k_1^2\mu_h\gamma_v k_7}w_9 < 0,$$

$$w_3 = \frac{\beta^*_{hv}\Lambda_h k_9(\mu_h + k_1\pi)}{k_1k_2k_7\gamma_v}w_9 > 0,$$

$$w_4 = \frac{\beta^*_{hv}\Lambda_h\gamma_h k_9(\mu_h + k_1\pi)}{k_1k_2k_3k_7\gamma_v}w_9 > 0,$$

$$w_5 = \frac{\beta^*_{hv}\Lambda_h\sigma\gamma_h k_9(\mu_h + k_1\pi)}{k_1k_2k_3k_7\mu_h\gamma_v}w_9 > 0,$$

$$w_7 = -\frac{\beta_{vh}\mu_h K\theta}{\mu_v k_7}\left(1 - \frac{1}{\mathcal{N}}\right)(\eta_h w_3 + w_4) < 0,$$

$$w_8 = \frac{\beta_{vh}\mu_h K\theta}{\mu_v k_4 k_7}\left(1 - \frac{1}{\mathcal{N}}\right)(\eta_h w_3 + w_4) > 0,$$

$$w_6 = \frac{\mu_b}{k_6\mathcal{N}^2}(w_7 + w_8 + w_9) \text{ and } w_9 > 0.$$

Similarly, $J(P_1)$ has a left eigenvector $\mathbf{v} = (v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8, v_9)$ where

$$v_1 = v_2 = v_5 = v_6 = v_7 = 0,\ v_3 = \frac{\mu_v k_1 k_7}{\beta_{vh}\Lambda_h k_8}v_9,$$

$$v_4 = \frac{\beta_{vh}K\theta\mu_h(\eta_v\mu_v + \gamma_v)}{k_3k_4k_7\mu_v}\left(1 - \frac{1}{\mathcal{N}}\right)v_9,$$

$$v_8 = \frac{(\eta_v\mu_v + \gamma_v)}{k_4}v_9 \text{ and } v_9 > 0.$$

a) Computation of $a^\star$: Using the non–zero components of $\mathbf{v}$ and the associated non–zero partial derivatives of f (at the DFE P_1), for system (3), we obtain

$$a^\star = \frac{1}{2}v_3\sum_{i,j=1}^{9} w_iw_j\frac{\partial^2 f_3(0,0)}{\partial x_i\partial x_j} + \frac{1}{2}v_8\sum_{i,j=1}^{9} w_iw_j\frac{\partial^2 f_8(0,0)}{\partial x_i\partial x_j}.$$

We finally obtain (See the details in appendix E)

$$a^\star = \phi_1 - \phi_2$$

where

$$\phi_1 = \frac{1}{2}v_3\left\{\frac{\beta^*_{hv}\mu_h}{k_1(\Lambda_h+m\mu_h)^2}\left[(\epsilon\xi\Lambda_h+m\mu_h)\left(w_1+\pi\, w_2\right)\right.\right.$$
$$\times\left(w_8\eta_v+w_9+\eta_v+1\right)$$
$$\left.\left.-2\Lambda_h(\mu_h+\pi\xi)\left(w_3+w_4+w_5\right)\left(w_8\eta_v+w_9\right)\right]\right\}$$
$$-\frac{1}{2}v_8\frac{\beta_{vh}\mu_h^2K\theta}{\mu_v(\Lambda_h+\mu_hm)^2}\left(1-\frac{1}{\mathcal{N}}\right)w_5\left(\eta_hw_3+w_4\right)$$
$$+\frac{1}{2}v_8\frac{\beta_{vh}\mu_h}{(\Lambda_h+\mu_hm)}\left(\eta_hw_3+w_4\right)w_7$$
$$-\frac{1}{2}v_8\frac{\beta_{vh}\mu_h^2K\theta\left(1-\frac{1}{\mathcal{N}}\right)}{\mu_v(\Lambda_h+\mu_hm)^2}$$
$$\times\left[2(\eta_h+1)w_3w_4+2\left(\eta_hw_3^2+w_4^2\right)\right]$$
$$<0$$

and

$$\phi_2 = \frac{1}{2}v_8\frac{\beta_{vh}\mu_h^2K\theta}{\mu_v(\Lambda_h+\mu_hm)^2}\left(1-\frac{1}{\mathcal{N}}\right)$$
$$\times\left[\left(\eta_hw_3+w_4\right)\left(w_1+w_2\right)\right]<0$$

b) Computation of $b^\star$:

$$b^\star = v_3\frac{\Lambda_h(\mu_h+\pi\xi)}{k_1(\Lambda_h+\mu_hm)}\left(\eta_vw_8+w_9\right)>0.$$

Since $b^\star>0$ according to the sign of w_i, v_i, for $i\in\{1\ldots,9\}$, we conclude that the backward bifurcation phenomenon may occurs if $a^\star>0$. We can summarize the results obtained above in the following theorem:

Theorem 4.1: If $a^\star>0$, then model (3) exhibits backward bifurcation at $R_0=1$. If the reversed inequality holds, then the bifurcation at $R_0=1$ is forward.

This is illustrated by simulating the model with different set of parameter values (it should be stated that these parameters are chosen for illustrative purpose only, and may not necessarily be realistic epidemiologically):

—Using the parameters values in Table II, except $\mu_v=\mu_1=\mu_2=1/14$, $\Lambda_h=200$, $\epsilon=0.80$, $\xi=0.475$, $\delta=0.6$, $\tilde{\beta}_{hv}=6$, $\tilde{\beta}_{vh}=50$ and $K=1000$ such that $R_0=0.6095<1$ and $a^\star=1.0348\times10^{-5}>0$, the numerical resolution of equation (44) (see appendix A), gives the following solution: $\lambda^*_{1h}=0$, $\lambda^*_{2h}=0.0083$, $\lambda^*_{3h}=10.9412$, $\lambda^*_{4h}=-0.0080$ and $\lambda^*_{5h}=-0.0001$; Note that the first solution $\lambda^*_{1h}=0$ corresponds to the disease free equilibrium. The second, and third solution, $\lambda^*_{2h}=0.0083$, $\lambda^*_{3h}=10.9412$, correspond to endemic equilibria; $\lambda^*_{2h}=0.0083$ correspond to unstable endemic equilibrium and $\lambda^*_{3h}=10.9412$ corresponds to the stable endemic equilibrium. The fourth and fifth solution $\lambda^*_{4h}=-0.0080$ and $\lambda^*_{5h}=-0.0001$ are not biologically meaningful.

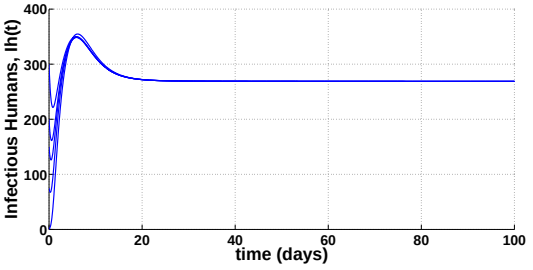

Fig. 1. Time profile of infectious humans using different initial conditions showing that the equilibrium $\lambda^*_{3h}=10.9412$ is stable even if $R_0=0.6095<1$.

—Using the parameters values in Table II, except $\mu_v=\mu_1=\mu_2=1/14$, $\Lambda_h=100$, $\epsilon=0.80$, $\xi=0.475$, $\delta=0.6$, $\tilde{\beta}_{hv}=4.0385$, $\tilde{\beta}_{vh}=100$ and $K=1000$ such that $R_0=1$ and $a^\star=2.3665\times10^{-4}>0$, the numerical resolution of equation (44), gives the following solution: $\lambda^*_{11h}=0$, $\lambda^*_{22h}=0.0114$, $\lambda^*_{3h}=8.5310$, and $\lambda^*_{44h}=-0.0111$; The first solution $\lambda^*_{1h}=0$ corresponds to the disease free equilibrium. The second, and third solution, $\lambda^*_{2h}=0.0083$, $\lambda^*_{33h}=8.5310$, correspond to endemic equilibria; $\lambda^*_{22h}=0.0114$ correspond to unstable endemic equilibrium and $\lambda^*_{33h}=8.5310$ corresponds to the stable endemic equilibrium. The fourth solution $\lambda^*_{4h}=-0.0111$ is not biologically meaningful.

—In the absence to disease induced death ($\delta=0$) and choosing $\tilde{\beta}_{hv}=4.0188$ and $K=1000$ such that $R_0=1$, equation (44) admit only one solution $\lambda^*_h=0$ which corresponds to the disease–free equilibrium. In this case, the backward bifurcation phenomenon does not occurs.

—Choosing $\tilde{\beta}_{hv}=10$ and $K=1000$ such that $R_0=1.630976>1$ and $a^\star=-1.8011<0$, equation (44) admit only one positive solution given by $\lambda^*_{1h}=0.0001$, which correspond to the

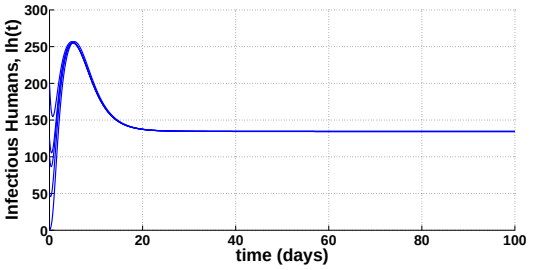

Fig. 2. Time profile of infectious humans using different initial conditions showing that the equilibrium $\lambda^*_{33h} = 8.5310$ is stable even if $R_0 = 1$.

endemic equilibria when the basic reproduction number, R_0, is greater than 1.

To conclude, depending to the values of parameters of model (3), the phenomenon of backward bifurcation may occurs when the classical basic reproduction number R_0 is less than unity.

V. Threshold analysis and vaccine impact

Since a future dengue vaccine, for example, is expected to be imperfect, it is instructive to determine whether or not its widespread use in a community will be benefic (or not) [10], [40], [68]. Now, consider the following model (model 3 without vaccination).

$$\begin{aligned}
\dot{S}_h &= \Lambda_h - \lambda_h S_h - \mu_h S_h \\
\dot{E}_h &= \lambda_h S_h - (\mu_h + \gamma_h) E_h \\
\dot{I}_h &= \gamma_h E_h - (\mu_h + \delta + \sigma) I_h \\
\dot{R}_h &= \sigma I_h - \mu_h R_h \\
\dot{A}_v &= \mu_b \left(1 - \frac{A_v}{K}\right)(S_v + E_v + I_v) - (\theta + \mu_A) A_v \\
\dot{S}_v &= \theta A_v - \lambda_v S_v - \mu_v S_v \\
\dot{E}_v &= \lambda_v S_v - (\mu_1 + \gamma_v) E_v \\
\dot{I}_v &= \gamma_v E_v - \mu_2 I_v
\end{aligned} \tag{19}$$

with λ_h and λ_v defined at (1) and (2), respectively. Following procedure in [26], [82], the corresponding basic reproduction number of model (19), R_s, is given by

$$\begin{aligned}
R_s^2 = &\frac{\beta_{hv}\beta_{vh} K \theta (k_3\eta_h + \gamma_h)(\gamma_v + \eta_v\mu_2)}{\mu_v\mu_2(\mu_h + \gamma_h)(\mu_h + \delta + \sigma)(\mu_1 + \gamma_v)} \\
&\times \frac{\Lambda_h \mu_h}{(\Lambda_h + m_m u_h)^2}\left(1 - \frac{1}{\mathcal{N}}\right)
\end{aligned} \tag{20}$$

So we deduce that

$$R_{vac} := R_0 = R_s \sqrt{\frac{(\pi\xi + \mu_h)}{(\mu_h + \xi)}}. \tag{21}$$

From Eq. (21), it follows that, in the absence of vaccination ($\xi = 0$) or when the vaccine efficacy is very low ($\epsilon \to 0$), we have $R_{vac} = R_s$. However, when humans vaccination comes to play, the basic reproductive number is reduced by a factor of $\sqrt{\frac{(\pi\xi + \mu_h)}{(\mu_h + \xi)}} < 1$. Since increasing vaccination efforts results in decreasing the magnitude of arboviruses infection, humans vaccination can contribute to control the spread of arboviral diseases. In the following, we use the set of parameters values given in Table III, which refer to Dengue and Chikungunya. Figs. 3–5 show several simulations, by varying the vaccine efficacy and the percentage of population that is vaccinated. Figure 3 shows simulations with different proportions of succeptible human vaccinated, using an imperfect vaccine, with a level of efficacy of 60%. Both total number of infected humans and infected vectors reache a peack after 25 days approximatively. However, when $\epsilon = 60\%$, the variation of vaccine coverage parameter have not a great impact in the number of infected humans and vectors. Figure 4 illustrates the effect of vaccine efficacy in the reduction of the total number of infected humans and vectors. It is clear that the effectiveness of the vaccine has a great impact when $\epsilon \geq 90\%$. Thus, it is suitable to add to vaccination (when $\epsilon < 90\%$) another control, such as, treatment of infected individuals, personal protection, and vector control strategies to stop the spread of arboviral diseases. Figure 5 shows the representation of the basic reproduction number R_0 plotted as function of the vaccine efficacy parameter ϵ and the proportion

TABLE III
BASELINE VALUES OF PARAMETERS OF MODEL (3) AND THEIR SOURCES.

Parameter	Baseline value	Sources
Λ_h	2.5 day^{-1}	[40]
ξ	variable	
ϵ	Variable	
η_h, η_v	0.35	Assumed
$\tilde{\beta_{hv}}$	0.75 day^{-1}	[40]
$\tilde{\beta_{hv}}$	0.75 day^{-1}	[40]
γ_h	1/3 day^{-1}	[30]
γ_v	1/2 day^{-1}	[30]
μ_h	$\frac{day^{-1}}{(71 \times 365)}$	[68]
μ_v	(1/14) day^{-1}	[40]
μ_A	1/5 day^{-1}	[30]
μ_1^{-1}	10 days	[30]
μ_2^{-1}	5 days	[30]
θ	0.08 day^{-1}	[30], [68]
δ	10^{-3} day^{-1}	[40]
σ	0.1428 day^{-1}	[2], [40]
a	1 day^{-1}	[40], [61]
m	100	Assumed
K	2×5000	Assumed
μ_b	6 day^{-1}	[68], [60], [61]

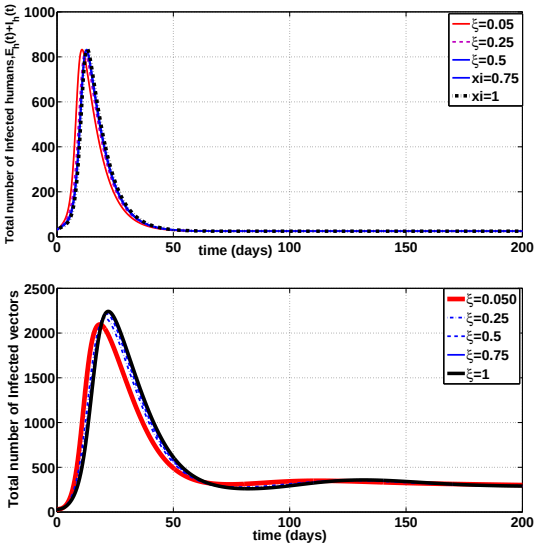

Fig. 3. Total number of infected humans and vectors varying the proportion of susceptible huamans vaccinated $\xi = (0.05; 0.25; 0.5; 0.75; 1)$ with a vaccine simulating 60% of effectiveness (i.e. $\epsilon = 0.60$ or $\pi = 1 - \epsilon = 0.4$).

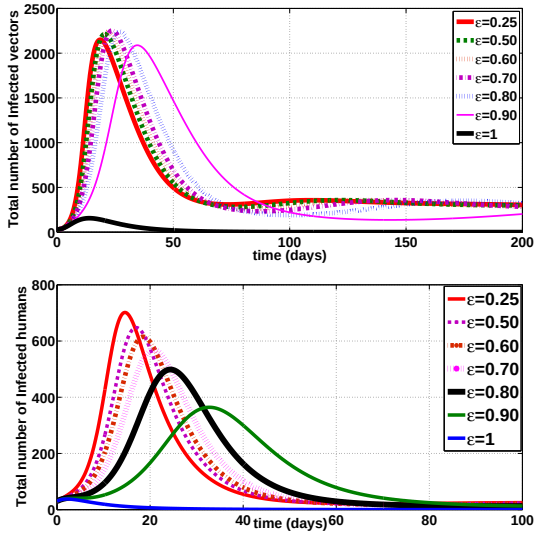

Fig. 4. Infected humans and Vector varying the efficacy level of the vaccine $\epsilon = (0.25; 0.50; 0.80; 0.90; 1)$ and considering that 85% of susceptible humans is vaccinated.

of susceptible population vaccinated ξ. The use of a vaccine with level of efficacy greather than 90% approximatively, dramaticaly decrease the basic reproduction number, when the proportion of susceptible humans vaccinated are greather than 85%. We observe the same result at Figure 6. Thus, the use of a vaccine with a high level of efficacy and a wide vaccine coverage has an impact on stopping the spread of the disease. However, if the vaccine efficacy is not high, it is important to add another control strategies. Our sensitive analysis in later section will further support this result.

VI. SENSITIVITY ANALYSIS

To determine the best way to fight against arboviruses, it is necessary to know the relative importance of the various factors responsible for their transmission in both the human population than in the vector population, as well as effective means to fight these diseases. The transmission of the disease is directly related to R_0, and the prevalence of the disease is directly related to the infected states, especially for sizes of $E_h(t)$, $I_h(t)$, $E_v(t)$ and $I_v(t)$. These variables are relevant to

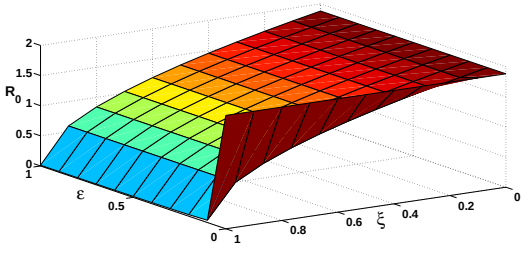

Fig. 5. The basic reproduction number R_0 plotted as function of the vaccine efficacy parameter ϵ and the proportion of susceptible population vaccinated ξ. The set of parameter values is given in Table III.

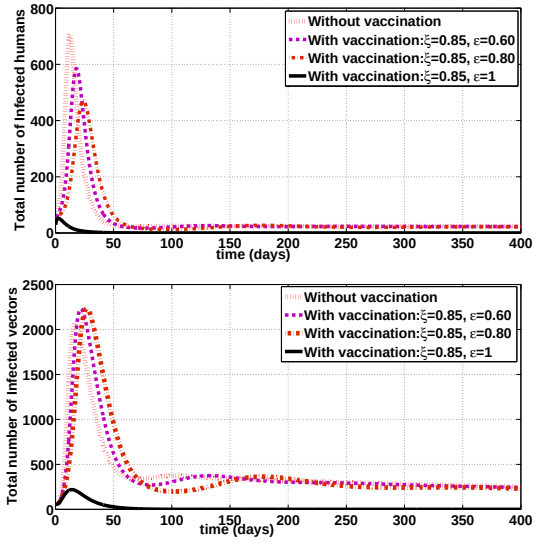

Fig. 6. Time profile of total number of infected human and vector without vaccination and with vaccination.

the individuals (humans and vectors) who have some life stage of arboviruses in their bodies. The number of infectious humans, I_h, is especially important because it represents the people who may be clinically ill, and is directly related to the total number of arboviral deaths [22]. We will perform a global sensitivity analysis.

A. Mean values of parameters and initial values of variables

Since we focus in this article, to a general model of arboviral diseases, we will, in this section, use the parameters values of two particular arboviruses, Dengue and Chikungunya. It is important to note that these two diseases are transmitted by the same mosquito: *Aedes albopictus. However, dengue is also transmited by Aedes aegypti* [30], [35], [36], [38], [40], [61], [68], [90].

The mean values of parameters are listed in Table III, the range values of parameters are in Table IV and the initial conditions are given in Table V.

TABLE IV
PARAMETER VALUE RANGES OF MODEL (3) USED AS INPUT FOR THE LHS METHOD.

Parameter	Range	Parameter	Range
Λ_h	[1 , 6]	μ_A	[1/10,1/4]
ξ	[0.05,1]	μ_1	[1/21,1/3]
ϵ	[0.5,0.9]	μ_2	[1/21,1/3]
η_h, η_v	[0.1,0.8]	θ	[0.01,0.17]
$\tilde{\beta_{hv}}$	[0.375,1]	δ	$[10^{-5},10^{-2}]$
$\tilde{\beta_{vh}}$	[0.375,1]	σ	[0.1428,1/3]
γ_h	[1/12,1/2]	a	[1,3]
γ_v	[1/21,1/2]	m	[1,201]
μ_h	$\left[\frac{1}{78\times 365}, \frac{1}{45\times 365}\right]$	K	$10^3\times$[10,15]
μ_v	[1/21,1/10]	μ_b	[6,18]

TABLE V
INITIAL CONDITIONS.

Human	Initial value	vector	Initial value
S_h:	1000	A_v	1000
V_h:	0	S_v:	500
E_h:	20	E_v:	20
I_h:	10	I_v:	40
R_h:	0		

B. Uncertainty and sensitivity analysis

1) Sensitivity analysis of R_0: We study the impact of each parameter of the model on the value of the basic reproduction number R_0. Following the approach of Wu and colleagues [88], we perform the analysis by calculating the Partial Rank Correlation Coefficients (PRCC) between each parameter of our model and the basic reproduction number, R_0. Table III troughly estimates

the mean value for each parameter. It is important to notice that, variations of these parameters in our deterministic model lead to uncertainty to model predictions since the basic reproductive number varies with parameters. Due to the absence of data on the distribution function, a uniform distribution is chosen for all parameters. The sets of input parameter values sampled using the Latin Hypercube Sampling (LHS) method were used to run 1,000 simulations.

With these 1,000 runs of Latin Hypercube Sampling, the derived sampling distribution of R_0 is shown in Figure 7. From this sampling we get that the mean of R_0 is 1.9304 and the standard deviation is 1.6128. Hence, statistically we are very confidential that model (3) is in an endemic state since $R_0 > 1$.

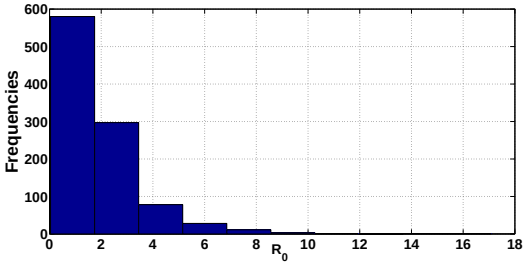

Fig. 7. Sampling distribution of R_0 from 1,000 runs of Latin hypercube sampling. The mean of R_0 is 1.9304 and the standard deviation is 1.6128.

From the previous sampling we compute the Partial Rank Correlation Coefficients between R_0 and each parameter of model (3). The result is displayed in Table VI. According to Boloye Gomero [13], the parameters with large PRCC values (> 0.5 or < -0.5) as well as corresponding small p-values (< 0.05) are most influential in model (3).

Table VI show that the parameter ϵ have the highest influence on the reproduction number R_0. Although ϵ is the vaccine efficacy. This suggests that the development of a vaccine with high level of efficacy may potentially be an effective strategy to reduce R_0. The other parameters with an important effect are θ, a, Λ_h and μ_2. The parameters

TABLE VI
PRCC BETWEEN R_0 AND EACH PARAMETER.

Parameter		Correlation Coefficients	P–values
1	Λ_h	*–0.6067	$1.4578E-99$
2	ξ	0.0529	0.0977
3	ϵ	***–0.8043	$2.6732E-223$
4	η_h	0.2879	$4.0576E-20$
5	$\tilde{\beta_{hv}}$	0.4354	$1.3609E-46$
6	γ_h	–0.2598	$1.4099E-16$
7	μ_h	0.2526	$9.9492E-16$
8	δ	–0.0386	0.2274
9	σ	–0.3269	$7.7785E-26$
10	η_v	0.2039	$1.1635E-10$
11	$\tilde{\beta_{vh}}$	0.4215	$1.7130E-43$
12	γ_v	0.2117	$2.1787E-11$
13	μ_v	–0.3029	$3.0015E-22$
14	μ_A	–0.0121	0.7049
15	μ_1	–0.2948	$4.2501E-21$
16	μ_2	*–0.5087	$1.2669E-65$
17	θ	**0.7626	$3.0823E-187$
18	a	**0.7134	$3.4096E-153$
19	m	–0.0436	0.1724
20	K	0.3880	$1.4683E-36$
21	μ_b	0.0082	0.7973

which do not have almost any effect on R_0 are ξ, δ, μ_A, m and μ_b. In particular, the least sensitive parameters is μ_b, the number of eggs at each deposit per capita.

2) Sensitivity analysis of Infected states of model (3)*:* With 1,000 runs of Latin hypercube sampling, we compute the PRCC between infected states $E_h(t)$, $I_h(t)$, $E_v(t)$, and $I_v(t)$ and each parameter of model (3). The result is displayed in Tables VII–X. As in Table VI, the parameters with large PRCC values (> 0.5 or < -0.5) as well as corresponding small p-values (< 0.05) are most influential in model (3).

From Tables VII–X, we can observe the following facts:

–For the value of E_h, the parameters with more influence are θ, K, a, ϵ, Λ_h and μ_2. The parameters which do not have almost any effect on the variation of E_h are μ_h, δ, μ_A, m and μ_b. In particular, the least sensitive parameters is μ_b, the number of eggs at each deposit per capita;

–For the value of I_h, the parameters with more influence are Λ_h and γ_h. The least sensitive pa-

TABLE VII
PRCC BETWEEN INFECTED HUMANS E_h AND EACH PARAMETER.

Parameter		Correlation Coefficients	P–values
1	Λ_h	**0.6842	$3.2080E-136$
2	ξ	0.4115	$2.4590E-41$
3	ϵ	***0.7177	$6.8762E-156$
4	η_h	–0.2457	$6.1306E-15$
5	$\tilde{\beta}_{hv}$	–0.4215	$1.7187E-43$
6	γ_h	0.2172	$6.2865E-12$
7	μ_h	0.0086	0.7879
8	δ	-0.0259	0.4176
9	σ	0.3395	$7.4246E-28$
10	η_v	–2378	$4.5858E-14$
11	$\tilde{\beta}_{vh}$	–0.4232	$7.4972E-44$
12	γ_v	–0.2311	$2.4083E-13$
13	μ_v	0.2906	$1.5881E-20$
14	μ_A	0.0210	0.5122
15	μ_1	0.3340	$5.8090E-27$
16	μ_2	*0.5747	$3.1691E-87$
17	θ	***–0.7599	$3.7832E-185$
18	a	***–0.7597	$4.9923E-185$
19	m	0.0537	0.0931
20	K	***–0.7477	$4.2124E-176$
21	μ_b	–0.0068	0.8328

TABLE VIII
PRCC BETWEEN INFECTIOUS HUMANS I_h AND EACH PARAMETER.

Parameter		Correlation Coefficients	P–values
1	Λ_h	***0.8727	$9.1342E-307$
2	ξ	0.0078	0.8062
3	ϵ	–0.2887	$2.8614E-20$
4	η_h	0.0711	0.0261
5	$\tilde{\beta}_{hv}$	0.0850	0.0078
6	γ_h	***–0.8722	$5.9181E-306$
7	μ_h	–0.0363	0.2566
8	δ	0.0412	0.1978
9	σ	–0.0531	0.0965
10	η_v	0.0310	0.3316
11	$\tilde{\beta}_{vh}$	0.1297	$4.6364E-5$
12	γ_v	–0.0179	0.5764
13	μ_v	–0.0544	0.0886
14	μ_A	–0.0222	0.4877
15	μ_1	–0.0580	0.0697
16	μ_2	–0.0423	0.1855
17	θ	0.1312	$3.7931E-5$
18	a	0.1428	$2.8933E-6$
19	m	–0.0017	0.9586
20	K	0.1783	$1.9260E-8$
21	μ_b	–0.0054	0.8648

TABLE IX
PRCC BETWEEN INFECTED VECTORS E_v AND EACH PARAMETER.

Parameter		Correlation Coefficients	P–values
1	Λ_h	–0.0186	0.5603
2	ξ	–0.0111	0.7280
3	ϵ	0.0135	0.6723
4	η_h	–0.1086	$6.6203E-4$
5	$\tilde{\beta}_{hv}$	–0.0664	0.0375
6	γ_h	0.0560	0.0798
7	μ_h	–0.0295	0.3563
8	δ	0.0116	0.7170
9	σ	0.0734	0.0215
10	η_v	–0.0273	0.3928
11	$\tilde{\beta}_{vh}$	–0.0913	0.0043
12	γ_v	0.0069	0.8282
13	μ_v	**-0.5923	$7.6830E-94$
14	μ_A	0.0157	0.6235
15	μ_1	0.0331	0.3006
16	μ_2	0.0043	0.8933
17	θ	***0.9225	0
18	a	–0.0822	0.0100
19	m	0.0027	0.9324
20	K	***0.9199	0
21	μ_b	0.1125	$4.1594E-4$

TABLE X
PRCC BETWEEN INFECTIOUS VECTORS I_v AND EACH PARAMETER.

Parameter		Correlation Coefficients	P–values
1	Λ_h	0.2254	$9.3729E-13$
2	ξ	–0.0090	0.7785
3	ϵ	–0.1228	$1.1697E-4$
4	η_h	0.3126	$1.1661E-23$
5	$\tilde{\beta}_{hv}$	0.0031	0.9216
6	γ_h	–0.3233	$2.7921E-25$
7	μ_h	0.0381	0.2338
8	δ	–0.0215	0.5015
9	σ	–0.3869	$2.4025E-36$
10	η_v	0.0196	0.5402
11	$\tilde{\beta}_{vh}$	0.5584	$2.0585E-109$
12	γ_v	–0.6287	$6.0859E-109$
13	μ_v	–0.4856	$4.0722E-59$
14	μ_A	0.0294	0.3583
15	μ_1	–0.4380	$3.3922E-47$
16	μ_2	–0.0103	0.7470
17	θ	**0.8728	$7.6088E-307$
18	a	*0.6011	$2.5895E-97$
19	m	–0.0640	0.0451
20	K	*0.8600	$5.9602E-288$
21	μ_b	–0.0770	0.0159

rameters is μ_b, the number of eggs at each deposit per capita;

–For the value of E_v, the parameters with more influence are the maturation rate from larvae to adult θ, and the capacity of breeding sites K. The other parameter is the natural mortality rate of vector μ_v. The least sensitive parameters is m, the number of alternative source of blood;

–For the value of I_v, the parameters with more influence are θ, K, γ_v, a and $\tilde{\beta}_{vh}$. The least sensitive parameters is $\tilde{\beta}_{hv}$, the probability of transmission of infection from an infectious vector to a susceptible human.

Although the model is sensitive to the variations of the vaccine efficacy parameter ϵ, there are other parameters (such as θ, a, K, μ_v, μ_2) which have a considerable impact on the value of the basic reproduction number R_0 and the number of infected individuals. Thus, it is important to take into account other control strategies in the fight against arboviral diseases.

VII. Numerical simulation

In order to illustrate some of the results obtained in the previous sections, we provide here some numerical simulations. We use the nonstandard scheme given by (22). It is important to note that standard numerical methods may fail to preserve the dynamics of continuous models [4], [59], [81]. Generally, compartmental models are solved using standard numerical methods, for example, Euler or Runge Kutta methods included in software package such as Scilab [76] or Matlab [57]. These methods can sometimes lead to spurious behaviours which are not in adequacy with the continuous system properties that they aim to approximate. For example, they may lead to negative solutions, exhibit numerical instabilities, or even converge to the wrong equilibrium for certain values of the time discretization or the model parameters (see [3], [4], [5], [81] for further investigations).

A. A nonstandard scheme for the model (3)

Following [30], system (3) is discretized as follows:

$$\begin{cases} \dfrac{X_S^{k+1}-X_S^k}{\phi(h)} = \mathcal{A}_1(X^k)(X_S^k - X_{DFE}) \\ \qquad\qquad - D_{12}(X_I^k)X_S^{k+1} + B_{12}(X^k)X_I^k \\ \dfrac{X_I^{k+1}-X_I^k}{\phi(h)} = \mathcal{A}_2(X_S^{k+1})X_I^k \end{cases} \tag{22}$$

such that

$$-D_{12}(X_I)X_S + B_{12}(X)X_I = \mathcal{A}_{12}(X)X_I \tag{23}$$

with

$$D_{12}(X_I) = \begin{pmatrix} \lambda_h & 0 & 0 & 0 & 0 \\ 0 & \pi\lambda_h & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \lambda_v \end{pmatrix},$$

and

$$B_{12}(X) = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & \sigma & 0 & 0 & 0 \\ 0 & 0 & \mu_b\left(1-\dfrac{A_v^0}{K}\right) & \mu_b\left(1-\dfrac{A_v}{K}\right) & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

which implies that the scheme is consistant with formulation (11).

Rearranging (22), we obtain the foollowing new expression

$$\begin{cases} \mathcal{A}_k X^{k+1} = \mathcal{B}_k \\ X^k \geq 0 \end{cases} \tag{24}$$

with

$$\mathcal{A}_k = \begin{pmatrix} I_5 + \phi(h)D_{12}(X_I^k) & 0 \\ 0 & I_5 \end{pmatrix}$$

and

$$\mathcal{B}_k = \begin{pmatrix} X_S^k + \phi(h)\left[\mathcal{A}_1(X^k)(X_S^k - X_{DFE}) + B_{12}(X^k)X_I^k\right] \\ X_I^k\left[I_4 + \phi(h)\mathcal{A}_2(X_S^{k+1})\right] \end{pmatrix}.$$

where I_4 and I_5 are the identity matrix of order 4 and 5 respectively. Thus, we claim the following result:

Lemma 7.1: Our non-standard numerical scheme (22) is positively stable, i.e. for $X^k \geq 0$ we obtain $X^{k+1} \geq 0$, where $X^k = \left(S_h^k, V_h^k, E_h^k, I_h^k, R_h^k, A_v^k, S_v^k, E_v^k, I_v^k\right)^T$.

Proof: We suppose $X_k \geq 0$. $\mathcal{A}_k$ is a positive diagonal matrix and thus, $\mathcal{A}_k^{-1} \geq 0$. B_{12} is a positive matrix and we also have $-\mathcal{A}_1(X^k)X_{DFE} \geq 0$. To show that $\mathcal{B}_k$ is a positive matrix, it suffices to choose $\phi(h)$ such that

$$I_d + \phi(h)\mathcal{A}_1(X) \geq I_d + \phi(h)\underline{\mathcal{A}}_1 \geq 0,$$
$$I_d + \phi(h)\mathcal{A}_2(X) \geq I_d + \phi(h)\underline{\mathcal{A}}_2 \geq 0$$

where $\underline{\mathcal{A}}_1$ and $\underline{\mathcal{A}}_2$ are lower bounds for the sets $\{X \in \mathcal{D} | \mathcal{A}_1(X)\}$ and $\{X \in \mathcal{D} | \mathcal{A}_2(X)\}$ respectively. Following [30], to have $\mathcal{B}_k \geq 0$, it suffices to consider the following time-step function

$$\phi(h) = \frac{1 - e^{-Qh}}{Q} \tag{25}$$

with $Q \geq \max(k_1, k_2, k_3, \mu_h, k_4, k_6, \mu_v, \mu_2)$. We have proved that $X^k \geq 0$ implies $X^{k+1} \geq 0$. ■

Concerning the equilibria of our numerical scheme, we have the following result

Lemma 7.2: Our non-standard numerical scheme (22) and the continuous model (3) have the same equilibria.

Proof: See appendix F. ■

The stability of the trivial equilibrium is given by the foollowing result

Lemma 7.3: If $\phi(h)$ has choosen as equation (25), then the tivial equilibrium $TE := P_0$ is locally asymptotically stable for our numerical scheme (22) whenever $\mathcal{N} \leq 1$.

Proof: See appendix G. ■

Now, we also have the following result concerning the stability of the disease–free equilibrium:

Lemma 7.4: If $\phi(h)$ has choosen as equation (25) and $R_0 < 1$, then the disease–free equilibrium $DFE := P_1$ is locally asymptotically stable for our numerical scheme (22) .

Proof: The proof of Lemma 7.4 follows the proof of Proposition 3.4 in [30]. See also [5] for a proof in a more general setting. ■

B. Simulation Results

We now provide some numerical simulations to illustrate the theoretical results (local stability, global stability and backward bifurcation). We use parameters values given in Table III with $\xi = 0.475$, $\epsilon = 0.60$, $K = 1000$ and initial conditions given in Table V.

Figure 8 illustrates the asymptotic stability of the trivial equilbrium whenever the treshold $\mathcal{N}$ is less than unity. In Figure 9, when $\mathcal{N} > 1$ the trivial equilibrium is unstable and the disease–free equilibrium is stable (first panel). The phenomenon of backward bifurcation occurs in the second panel of figure 9, where the stable disease-free equilibrium of the model co–exists with a stable endemic equilibrium when the associated reproduction number, R_0, is less than unity. Figures 10–11 show the existence of at least one endemic equilibrium whenever R_0 is equal or greather than unity.

It is important to mentione that the simulation results discussed in this work are subject to the uncertainties (See section VI) in the estimates of the parameter values (tabulated in Table III) used in the simulations. The effect of such uncertainties on the results obtained can be assessed using a sampling technique, such as Latin Hypercube Sampling.

VIII. Conclusions

In this paper, we formulated a compartmental model which takes into account a future vaccination strategy in human population, the aquatic development stage of vector and the alternative sources of blood.

The analysis has been performed by means of stability, bifurcation and sensitivity analysis. We have obtained that the disease–induced mortality may be the main cause for the occurrence of the backward bifurcation (see remark 4.1). This means that relatively high values of disease–induced mortality rate may induce stable endemic states also when the basic reproduction number R_0 is below the classical threshold $R_0 = 1$. The stability analysis reveals that for $\mathcal{N} \leq 1$,

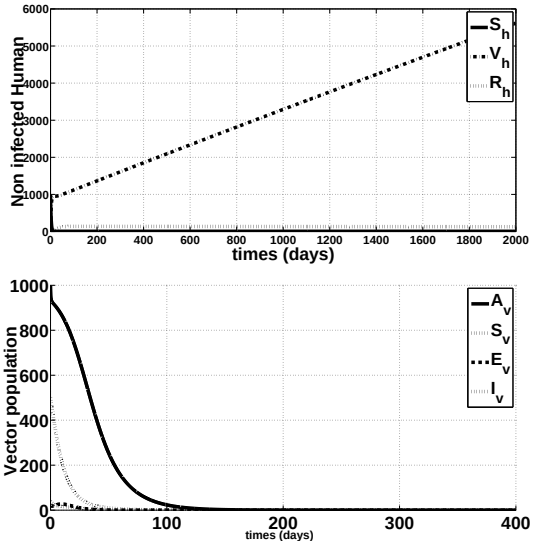

Fig. 8. Time profile of both population without vector (with $\theta = 0.0008$, so $\mathcal{N} = 0.2679 < 1$. In this case the trivial equilibrium is globally asymptotically stable.

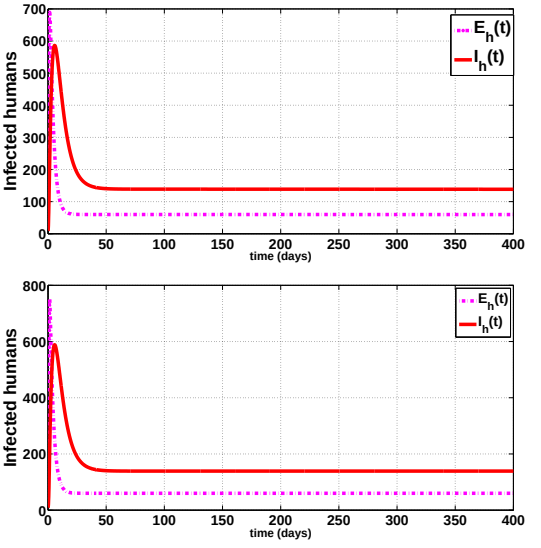

Fig. 10. Time profile of infected humans with $\tilde{\beta}_{hv} = 42.9631$, $\Lambda_h = 20$, so that $R_0 = 1$ (first panel) and $\tilde{\beta}_{hv} = \tilde{\beta}_{vh} = 20$, $\Lambda_h = 20$, so that $R_0 = 3.5233 > 1$ (second panel).

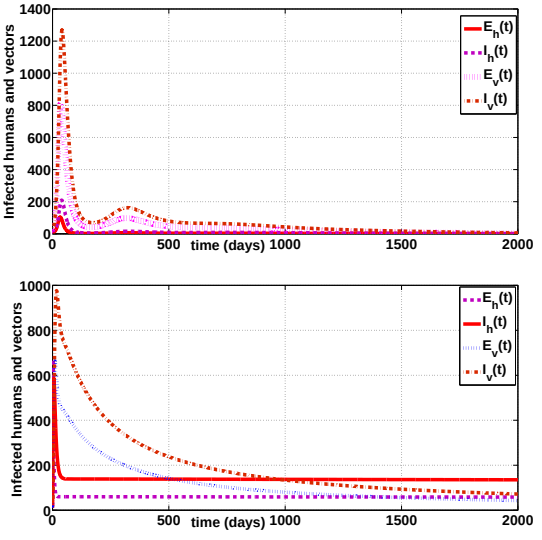

Fig. 9. Time profile infected humans and vectors. First panel:$R_0 =: 0.2377 < 1$ and Second panel: $R_0 = 0.9405 < 1$. The backward bifurcation phenomenon is illustrate in second panel.

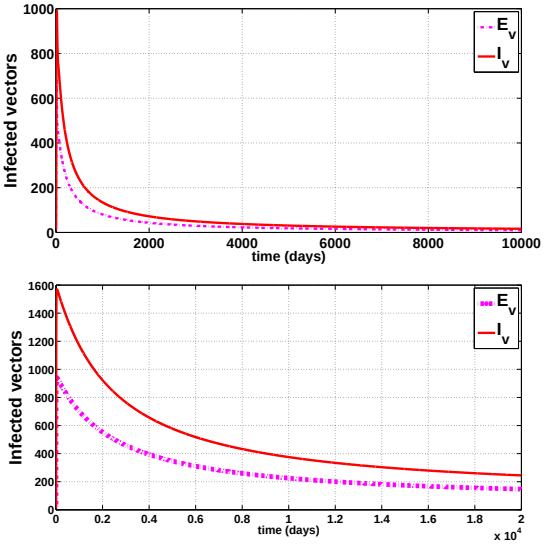

Fig. 11. Time profile of infected vectors with $\tilde{\beta}_{hv} = 42.9631$, $\Lambda_h = 20$, so that $R_0 = 1$ (first panel) and $\tilde{\beta}_{hv} = \tilde{\beta}_{vh} = 20$, $\Lambda_h = 20$, so that $R_0 = 3.5233 > 1$ (second panel).

the trivial equilibrium is globally asymptotically stable. When $\mathcal{N} > 1$ and $R_0 < 1$, the disease–free equilibrium is locally asymptotically stable. In the absence of disease-induced death, the disease–free equilibrium is also globally asymptotically

stable. The reduced version of the model (3) (in the absence of disease–induced mortality in both human and vector populations) have a unique endemic equilibrium point whenever its associated reproduction number $\mathcal{R}_1$ exceeds unity.

Taking as cases study the dengue and chikungunya transmission, we used parameter values from the literature to estimate statistically the basic reproduction number, R_0, and to perform a global sensitivity analysis on the basic reproduction number and infected states (E_h, I_h, E_v, I_v). Using Latin Hypercube Sampling, we obtain that the mean of R_0 is 1.9304. Hence, statistically we are very confident that our model (3) is in an endemic state. The global sensitivity analysis reveals that, apart from the parameters related to vaccination, particularly vaccine efficacy, other parameters (such as parameters related to vector population) also have a great impact on the basic reproduction number (R_0) and on the number of infected humans and vectors (E_h, I_h, E_v, I_v).

Numerical simulations of the model (3), using a nonstandard qualitatively stable scheme, show that the use of a vaccine with high level of efficacy has a proponderant role in the reduction of the disease spread. However, since the efficacy of the proposed vaccine for dengue, for example, has been around 60%, it is suitable to combine vaccination with other mechanisms of control.

Also, to be the best control strategy, the vaccination process must verify the following conditions:

(a) The vaccine must be approved by the relevant agencies (such as WHO, CDC), before its use.
(b) The vaccine efficacy should be high, as well as vaccine coverage.
(c) The price of the vaccine must be low for countries affected by the disease.

There are already governments, affected by the diseases, willing to use the vaccine before it is approved, which can have unpredictable consequences, so condition (a) does not hold. Moreover, according to previous analysis and french laboratory SANOFI, the condition (b) does not hold. Thus it is important to know what happens when we combine vaccination with other mechanisms of control already studied in the literature, such as personal protection, chemical interventions and education campaigns [30], [40], [60], [61], [63], [64], [67], [68], [69]. This is the perspective of our work.

ACKNOWLEDGMENT

Hamadjam ABBOUBAKAR and Léontine Nkague NKAMBA thank the Direction of UIT of Ngaoundéré and ENS of Yaoundé I, respectively, for their financial help granted under research missions in the year 2014. The authors are very grateful to two anonymous referees, for valuable remarks and comments, which significantly contributed to the quality of the paper.

APPENDIX

Appendix A: PROOF OF PROPOSITION 3.1

To find the equilibrium points of our system, we will solve the following system

$$\begin{cases} \Lambda_h - \lambda_h S_h - (\xi + \mu_h) S_h = 0 \\ \xi S_h - (1-\epsilon)\lambda_h V_h - \mu_h V_h = 0 \\ \lambda_h \left[S_h + (1-\epsilon) V_h\right] - (\mu_h + \gamma_h) E_h = 0 \\ \gamma_h E_h - (\mu_h + \delta + \sigma) I_h = 0 \\ \sigma I_h - \mu_h R_h = 0 \\ \mu_b \left(1 - \dfrac{A_v}{K}\right)(S_v + E_v + I_v) - (\theta + \mu_A) A_v = 0 \\ \theta A_v - \lambda_v S_v - \mu_v S_v = 0 \\ \lambda_v S_v - (\mu_1 + \gamma_v) E_v = 0 \\ \gamma_v E_v - \mu_2 I_v = 0 \end{cases} \tag{26}$$

To this aim, let $P^* = (S_h^*, E_h^*, I_h^*, R_h^*, A_v^*, S_v^*, E_v^*, I_v^*)$ represents any arbitrary endemic equilibrium of (3). Further, let

$$\lambda_h^* = \frac{\beta_{hv}(\eta_v E_v^* + I_v^*)}{(N_h^* + m)}, \quad \lambda_v^* = \frac{\beta_{vh}(\eta_h E_h^* + I_h^*)}{(N_h^* + m)}, \tag{27}$$

be the forces of infection of humans and vectors at steady state, respectively. Solving the first five

equations in (26) at steady state gives

$$\begin{aligned} S_h^* &= \frac{\Lambda_h}{k_1+\lambda_h^*},\ V_h^* = \frac{\xi\Lambda_h}{(k_1+\lambda_h^*)(\pi\lambda_h^*+\mu_h)},\\ E_h^* &= \frac{\Lambda_h\lambda_h^*(\pi\xi+\mu_h+\pi\lambda_h^*)}{k_2(k_1+\lambda_h^*)(\pi\lambda_h^*+\mu_h)},\\ I_h^* &= \frac{\gamma_h\Lambda_h\lambda_h^*(\pi\xi+\mu_h+\pi\lambda_h^*)}{k_2k_3(k_1+\lambda_h^*)(\pi\lambda_h^*+\mu_h)},\\ R_h^* &= \frac{\sigma\gamma_h\Lambda_h\lambda_h^*(\pi\xi+\mu_h+\pi\lambda_h^*)}{\mu_hk_2k_3(k_1+\lambda_h^*)(\pi\lambda_h^*+\mu_h)}. \end{aligned} \tag{28}$$

where $\pi = 1-\epsilon$, $k_1 = \mu_h+\xi$, $k_2 = \mu_h+\gamma_h$ and $k_3 = \mu_h+\sigma+\delta$. Solving the last three equations in (26) at steady state gives

$$\begin{aligned} S_v^* &= \frac{\theta A_v^*}{(\mu_v+\lambda_v^*)},\ E_v^* = \frac{\theta A_v^*\lambda_v^*}{k_4(\mu_v+\lambda_v^*)},\\ I_v^* &= \frac{\gamma_v\theta A_v^*\lambda_v^*}{\mu_2k_4(\mu_v+\lambda_v^*)}. \end{aligned} \tag{29}$$

where $k_4 = \mu_1+\gamma_v$.
Substituting (29) in the sixth equation of (26) gives

$$A_v^*\left\{\frac{\mu_b\theta}{\mu_2k_4}\left(1-\frac{A_v^*}{K}\right)\left(\frac{\mu_2k_4+k_5\lambda_v^*}{\mu_v+\lambda_v^*}\right)-k_6\right\}=0 \tag{30}$$

with $k_5 = \mu_2+\gamma_v$ and $k_6 = \theta+\mu_A$.

The trivial solution of (30) is $A_v^* = 0$. Substituting this solution in (29) gives $S_v^* = E_v^* = I_v^* = 0$. When $E_v^* = I_v^* = 0$, we also have $\lambda_h^* = 0$, thus $E_h^* = I_h^* = R_h^* = 0$, $S_h^* = \dfrac{\Lambda_h}{k_1}$ and $V_h^* = \dfrac{\xi\Lambda_h}{\mu_hk_1}$. Then we obtain the trivial equilibrium $P_0 = \left(\dfrac{\Lambda_h}{k_1}, \dfrac{\xi\Lambda_h}{\mu_hk_1}, 0,0,0,0,0,0,0\right)$.

Now we suppose that $A_v^* \neq 0$. The possible solution(s) of (30) is the solution(s) of the following equation

$$\frac{\mu_b\theta}{\mu_2k_4}\left(1-\frac{A_v^*}{K}\right)\left(\frac{\mu_2k_4+k_5\lambda_v^*}{\mu_v+\lambda_v^*}\right)-k_6=0 \tag{31}$$

The direct resolution of equation (31) gives

$$A_v^* = K\left(\frac{\mu_2\mu_b\theta k_4\left(1-\dfrac{1}{\mathcal{N}}\right)+\alpha\lambda_v^*}{\mu_b\theta(\mu_2k_4+k_5\lambda_v^*)}\right) \tag{32}$$

where $\mathcal{N} = \dfrac{\mu_b\theta}{\mu_vk_6}$ and $\alpha = \mu_b\theta k_5 - \mu_2k_4k_6$.

Let us first compute the equilibrium without Disease, i.e. $\lambda_h^* = \lambda_v^* = 0$ or $E_h = I_h = E_v = I_v = 0$. From (32), we obtain

$$A_v^0 := K\left(1-\frac{\mu_vk_6}{\mu_b\theta}\right) := K\left(1-\frac{1}{\mathcal{N}}\right) \tag{33}$$

Thus, the existence of vector is regulated by the threshold $\mathcal{N}$. If $\mathcal{N} \leq 1$, the system (3) correspond to human population of free vectors and the trivial equilibrium in this case is P_0.

Now we suppose that $\mathcal{N} > 1$. From (28) and (29) (with $\lambda_v^* = \lambda_v^* = 0$), we obtain the non trivial equilibrium or the disease–free equilibrium $P_1 = \left(S_h^0, V_h^0, 0,0,0, A_v^0, S_v^0, 0, 0\right)$, where

$$\begin{aligned} S_h^0 &= \frac{\Lambda_h}{k_1},\ V_h^0 = \frac{\xi\Lambda_h}{k_1\mu_h},\ A_v^0 = K\left(1-\frac{1}{\mathcal{N}}\right),\\ S_v^0 &= \frac{\theta}{\mu_v}A_v^0. \end{aligned}$$

Appendix B: Proof of Proposition 3.2

We consider the Jacobian matrix associated to model (3) at the equilibrium TE. we have

$$\mathcal{J}(TE) = \begin{pmatrix} -k_1 & 0 & 0 & 0 & 0 & 0 \\ \xi & -\mu_h & 0 & 0 & 0 & 0 \\ 0 & 0 & -k_2 & 0 & 0 & 0 \\ 0 & 0 & \gamma_h & -k_3 & 0 & 0 \\ 0 & 0 & 0 & \sigma & -\mu_h & 0 \\ 0 & 0 & 0 & 0 & 0 & -k_6 \\ 0 & 0 & 0 & 0 & 0 & \theta \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$\begin{pmatrix} 0 & -\dfrac{\beta_{hv}\eta_vS_h^0}{N_h^0+m} & -\dfrac{\beta_{hv}S_h^0}{N_h^0+m} \\ 0 & -\dfrac{\pi\beta_{hv}\eta_vV_h^0}{N_h^0+m} & -\dfrac{\pi\beta_{hv}V_h^0}{N_h^0+m} \\ 0 & \dfrac{\beta_{hv}\eta_vS_0}{N_h^0+m} & \dfrac{\beta_{hv}S_0}{N_h^0+m} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ \mu_b & \mu_b & \mu_b \\ -\mu_v & 0 & 0 \\ 0 & -k_4 & 0 \\ 0 & \gamma_v & -\mu_2 \end{pmatrix},$$

were $S_0 = S_h^0 + \pi V_h^0$. The eigenvalues of $\mathcal{J}(TE)$ are given by $\lambda_1 = \lambda_2 = -\mu_h$, $\lambda_3 = -k_1$, $\lambda_4 = -k_2$, $\lambda_5 = -k_3$, and λ_6, λ_7, λ_8, λ_9 are eigenvalues of the submatrix

$$\bar{\mathcal{J}} = \begin{pmatrix} -k_6 & \mu_b & \mu_b & \mu_b \\ \theta & -\mu_v & 0 & 0 \\ 0 & 0 & -k_4 & 0 \\ 0 & 0 & \gamma_v & -\mu_2 \end{pmatrix}.$$

The characteristic polynomial of $\bar{\mathcal{J}}$ is given by

$$\mathcal{P}(\lambda) = \lambda^4 + A_1\lambda^3 + A_2\lambda^2 + A_3\lambda + A_4 = 0 \quad (34)$$

where $A_1 = \mu_v + \mu_2 + k_4 + k_6$, $A_2 = k_6\mu_v(1-\mathcal{N}) + (k_4+\mu_2)(\mu_v+k_6) + \mu_2 k_4$, $A_3 = k_6\mu_v(1-\mathcal{N})(k_4+\mu_2) + \mu_2 k_4(\mu_v+k_6)$ and $A_4 = \mu_2 k_4(1-\mathcal{N})$. Thus, it is clear that all coefficients are always positive since $\mathcal{N} < 1$. Now we just have to verify that the Routh–Hurwitz criterion holds for polynomial $\mathcal{P}(\lambda)$. To this aim, setting

$$H_1 = A_1,\ H_2 = \begin{vmatrix} A_1 & 1 \\ A_3 & A_2 \end{vmatrix},\ H_3 = \begin{vmatrix} A_1 & 1 & 0 \\ A_3 & A_2 & A_1 \\ 0 & A_4 & A_3 \end{vmatrix},$$

$$H_4 = \begin{vmatrix} A_1 & 1 & 0 & 0 \\ A_3 & A_2 & A_1 & 1 \\ 0 & A_4 & A_3 & A_2 \\ 0 & 0 & 0 & A_4 \end{vmatrix} = A_4 H_3.$$

The Routh-Hurwitz criterion of stability of the trivial equilibrium T_E is given by

$$\begin{cases} H_1 > 0 \\ H_2 > 0 \\ H_3 > 0 \\ H_4 > 0 \end{cases} \Leftrightarrow \begin{cases} H_1 > 0 \\ H_2 > 0 \\ H_3 > 0 \\ A_4 > 0 \end{cases} \quad (35)$$

We have

$$H_1 = A_1 = \mu_v + \mu_2 + k_4 + k_6 > 0,$$

$$\begin{aligned} H_2 &= A_1A_2 - A_3 \\ &= (k_6 + k_4 + \mu_2)\mu_v^2 + \left(\mu_2 k_6\left(1 - \frac{\mu_b\theta}{\mu_2 k_6}\right)\right. \\ &\quad \left. + k_6^2 + 2k_4k_6 + \mu_2k_6 + k_4^2 + 2\mu_2k_4 + \mu_2^2\right)\mu_v \\ &\quad + \mu_2k_6^2\left(1 - \frac{\mu_b\theta}{\mu_2k_6}\right) + k_4k_6^2 + (k_4+\mu_2)^2k_6 \\ &\quad + \mu_2k_4^2 + \mu_2^2k_4, \end{aligned}$$

$$\begin{aligned} H_3 &= A_1A_2A_3 - A_1^2A_4 - A_3^2 \\ &= (k_4+\mu_2)(\mu_v+k_6) \\ &\quad \times \left(k_6\mu_v(1-\mathcal{N}) + \mu_2\mu_v + \mu_2k_6 + \mu_2^2\right) \\ &\quad \times \left(k_6\mu_v(1-\mathcal{N}) + k_4\mu_v + k_4k_6 + k_4^2\right), \end{aligned}$$

Using inequality $1/\mu_2 \le 1/\mu_1 \le 1/\mu_v$, we obtain $H_2 > 0$. $H_3 > 0$ if $\mathcal{N} < 1$; $A_4 > 0$ if and only if $\mathcal{N} < 1$. Thus we conclude that the trivial equilibrium is locally asymptotically stable.

Now we assume that $\mathcal{N} > 1$. Following the procedure and the notation in [82], we may obtain the basic reproduction number R_0 as the dominant eigenvalue of the *next–generation matrix* [26], [82]. Observe that model (3) has four infected populations, namely E_h, I_h, E_v, I_v. It follows that the matrices F and V defined in [82], which take into account the new infection terms and remaining transfer terms, respectively, are given by

$$F = \frac{1}{N_h^0 + m} \times \begin{pmatrix} 0 & 0 & \beta_{hv}\eta_v S_0 & \beta_{hv}S_0 \\ 0 & 0 & 0 & 0 \\ \beta_{vh}\eta_h S_v^0 & \beta_{vh}S_v^0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

with $N_h^0 = \dfrac{\Lambda_h}{\mu_h}$,

$$V = \begin{pmatrix} (\mu_h+\gamma_h) & 0 & 0 & 0 \\ -\gamma_h & (\mu_h+\delta+\sigma) & 0 & 0 \\ 0 & 0 & (\mu_1+\gamma_v) & 0 \\ 0 & 0 & -\gamma_v & \mu_2 \end{pmatrix},$$

and the dominant eigenvalue of the next–generation matrix FV^{-1} is given by Eq. (10).

The local stability of the disease–free equilibrium P_1 is a direct consequence of Theorem 2 of [82]. This ends the proof.

Appendix C: Proof of Proposition 3.3

Setting Y=X-TE with $X = (S_h, V_h, E_h, I_h, R_h, A_v, S_v, E_v, I_v)^T$, we can rewrite (3) in the following manner

$$\frac{dY}{dt} = \mathcal{B}(Y)Y \quad (36)$$

where

$$\mathcal{B}(Y)=\begin{pmatrix} -\lambda_h-k_1 & 0 & 0 & 0 & 0 \\ \xi & -\pi\lambda_h-\mu_h & 0 & 0 & 0 \\ \lambda_h & \pi\lambda_h & -k_2 & 0 & 0 \\ 0 & 0 & \gamma_h & -k_3 & 0 \\ 0 & 0 & 0 & \sigma & -\mu_h \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$\begin{pmatrix} 0 & 0 & -\frac{\beta_{hv}\eta_v S_h^0}{N_h+m} & -\frac{\beta_{hv}S_h^0}{N_h+m} \\ 0 & 0 & -\frac{\pi\beta_{hv}\eta_v V_h^0}{N_h+m} & -\frac{\pi\beta_{hv}V_h^0}{N_h+m} \\ 0 & 0 & \frac{\beta_{hv}\eta_v S_0}{N_h+m} & \frac{\beta_{hv}S_0}{N_h+m} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ -A_{66} & \mu_b & \mu_b & \mu_b \\ \theta & -\lambda_v-\mu_v & 0 & 0 \\ 0 & \lambda_v & -k_4 & 0 \\ 0 & 0 & \gamma_v & -\mu_2 \end{pmatrix},$$

with $S_0 = (S_h^0 + \pi V_h^0)$, $A_{66} = \left(k_6 + \mu_b\frac{S_v+E_v+I_v}{K}\right)$. It is clear that $Y = (0,0,0,0,0,0,0,0,0,0)$ is the only equilibrium. Then it suffices to consider the following Lyapunov function $\mathcal{L}(Y) =< g, Y >$ were $g = \left(1,1,1,1,1,1,\frac{k_6}{\theta},\frac{k_6}{\theta},\frac{k_6}{\theta},\frac{k_6}{\theta}\right)$. Straightforward computations lead that

$$\begin{aligned}\dot{\mathcal{L}}(Y) &=< g, \dot{Y} > \overset{\text{def}}{=} < g, \mathcal{B}(Y)Y > \\ &= -\mu_h(Y_1+Y_2+Y_3+Y_4+Y_5) - \delta Y_4 \\ &+ \frac{k_6\mu_v}{\theta}(\mathcal{N}-1)Y_7 + \frac{k_6\mu_1}{\theta}\left(\frac{\mu_b\theta}{k_6\mu_1}-1\right)Y_8 \\ &- \mu_b\frac{Y_6}{K}(Y_7+Y_8+Y_9) \\ &+ \frac{k_6\mu_2}{\theta}\left(\frac{\mu_b\theta}{k_6\mu_2}-1\right)Y_9\end{aligned}$$

Using the fact that $1/\mu_2 \le 1/\mu_1 \le 1/\mu_v$, we have $\frac{\mu_b\theta}{k_6\mu_1} - 1 \le 0$ and $\frac{\mu_b\theta}{k_6\mu_2} - 1 \le 0$, which implies that $\dot{\mathcal{L}}(Y) \le 0$ if $\mathcal{N} \le 1$. Moreover, the maximal invariant set contained in $\left\{\mathcal{L}|\dot{\mathcal{L}}(Y)=0\right\}$ is $\{(0,0,0,0,0,0,0,0,0,0)\}$. Thus, from Lyapunov theory, we deduce that $(0,0,0,0,0,0,0,0,0,0)$ and thus, $TE := P_0$, is GAS if $\mathcal{N} \le 1$.

Appendix D: PROOF OF PROPOSITION 4.1.

We compute now the endemic equilibrium, i.e. we are looking for an equilibrium such that $\lambda_h^* \neq 0$ and $\lambda_v^* \neq 0$. We assume that $\mathcal{N} > 1$.

From the sixth equation of (26), at equilibrium, we have

$$S_v^* + E_v^* + I_v^* = \frac{Kk_6A_v^*}{\mu_b(K-A_v^*)} \tag{37}$$

From the last third equations of (26), at equilibrium, we have

$$\mu_v S_v^* + \mu_1 E_v^* + \mu_2 I_v^* = \theta A_v^* \tag{38}$$

we will observe the following two cases.

a) Absence of disease–induced death in vector: The absence of disease–induced death in vector is traduce by the relation $\mu_v = \mu_1 = \mu_2$, then equation (38) becomes

$$S_v^* + E_v^* + I_v^* = \frac{\theta}{\mu_v}A_v^* \tag{39}$$

Equalling Eqs. (37) and (39) gives like before

$$A_v^0 := K\left(1-\frac{\mu_v k_6}{\mu_b\theta}\right) = K\left(1-\frac{1}{\mathcal{N}}\right). \tag{40}$$

Substituting A_v^* by A_v^0 in equation (29) gives

$$\begin{aligned} S_v^* &= \left(1-\frac{1}{\mathcal{N}}\right)\frac{K\theta}{(\mu_v+\lambda_v^*)}, \\ E_v^* &= \left(1-\frac{1}{\mathcal{N}}\right)\frac{K\theta\lambda_v^*}{k_4(\mu_v+\lambda_v^*)}, \\ I_v^* &= \left(1-\frac{1}{\mathcal{N}}\right)\frac{K\theta\gamma_v\lambda_v^*}{\mu_v k_4(\mu_v+\lambda_v^*)}. \end{aligned} \tag{41}$$

Replacing (41) in the expression of λ_h^* gives

$$\lambda_h^* = \frac{\beta_{hv}(\eta_v E_v^* + I_v^*)}{(N_h^*+m)} = k_{10}\frac{\lambda_v^*}{(\mu_v+\lambda_v^*)}\times \left(\frac{\beta_{hv}\mu_h k_2 k_3(k_1+\lambda_h^*)(\pi\lambda_h^*+\mu_h)}{k_2k_3k_7(k_1+\lambda_h^*)(\pi\lambda_h^*+\mu_h) - \delta\gamma_h\Lambda_h\lambda_h^*(k_8+\pi\lambda_h^*)}\right) \tag{42}$$

where $k_7 = (\Lambda_h + m\mu_h)$, $k_8 = \pi\xi + \mu_h$, $k_9 = \mu_2\eta_v + \gamma_v = \eta_v\mu_v + \gamma_v$ and $k_{10} = \frac{k_9K\theta}{\mu_v k_4}\left(1-\frac{1}{\mathcal{N}}\right)$.

Replacing (28) in the expression of λ_v^* gives

$$\lambda_v^* = \left(\frac{\beta_{vh}\Lambda_h\mu_h k_{11}\lambda_h^*(k_8+\pi\lambda_h^*)}{k_2k_3k_7(k_1+\lambda_h^*)(\pi\lambda_h^*+\mu_h) - \delta\gamma_h\Lambda_h\lambda_h^*(k_8+\pi\lambda_h^*)}\right) \tag{43}$$

where $k_{11} = k_3\eta_h + \gamma_h$.

Substituting (43) in (42) gives the following equation

$$f(\lambda_h^*) := \lambda_h^* \left[B_4(\lambda_h^*)^4 + B_3(\lambda_h^*)^3 + B_2(\lambda_h^*)^2 + B_1\lambda_h^* + B_0\right] = 0 \quad (44)$$

where

$$\begin{aligned}
B_4 &= \pi^2 \left[k_7(\mu_h k_3 + \gamma_h(\mu_h + \sigma)) + \delta\gamma_h m\mu_h\right] \\
&\quad \times \left\{\mu_v \left[k_7(\mu_h k_3 + \gamma_h(\mu_h + \sigma)) + \delta\gamma_h m\mu_h\right] \right. \\
&\quad \left. + \beta_{vh} k_{11}\Lambda_h\mu_h\right\} \\
B_3 &= 2\pi X \left\{k_2k_3k_7\mu_h(1+\pi) + \delta\gamma_h\Lambda_h\mu_h \right. \\
&\quad \left. + \pi\xi X\right\}\mu_v + \beta_{vh}\pi\Lambda_h\mu_h k_{11}\left\{\pi k_2k_3Y \right. \\
&\quad \left. + k_7\left[k_8(k_2k_3 - 2\delta\gamma_h) + \mu_h k_2k_3\right]\right\} \\
B_2 &= \mu_v\left[k_1k_2k_3k_7\pi - \delta\Lambda_h\gamma_h\pi\xi + X\mu_h\right]^2 \\
&\quad + 2k_1k_2k_3k_7\pi\mu_h\mu_v X \\
&\quad + \beta_{vh}\Lambda_h\mu_h^2\pi k_2k_3k_{11}\left\{\pi k_1k_7 \right. \\
&\quad \left. - \beta_{hv}k_{10}\left[\pi(k_8 + k_1) + \mu_h\right]\right\} \\
&\quad + \beta_{vh}k_8k_{11}\Lambda_h\mu_h\left[k_2k_3k_7\pi\mu_h + k_8X\right] \\
B_1 &= 2k_1k_2k_3k_7\mu_h\mu_v\left[k_8X + \pi\mu_h k_2k_3k_7\right] \\
&\quad + k_2k_3k_{11}\beta_{vh}\Lambda_h\mu_h^2\left\{k_1k_7k_8 \right. \\
&\quad \left. - \beta_{hv}k_{10}(\mu_h k_8 + k_1\pi(k_8 + \mu_h))\right\}
\end{aligned}$$

with $X = k_2k_3k_7 - \delta\gamma_h\Lambda_h$, $Y = k_1k_7 - \beta_{hv}\mu_h k_{10}$; and

$$B_0 = \mu_h^2\mu_v k_1^2k_2^2k_3^2k_7^2\left(1 - R_0^2\right)$$

We consider $\lambda_h^* \neq 0$, otherwise we recover DFE. The positive endemic equilibria $P^* = (S_h^*, V_h^*, E_h^*, I_h^*, R_h^*, A_v^*, S_v^*, E_v^*, I_v^*)$ are obtained by solving Eq. (44) for λ_h^*. The coefficient B_4 is always positive and coefficient B_0 is negative (resp. positive) whenever $R_0 > 1$ (resp. $R_0 < 1$). The number of possible nonnegative real roots of the polynomial of Eq. (44) depends on the signs of B_3, B_2 and B_1. The various possibilities for the roots of $f(\lambda_h^*)$ are tabulated in Table XI and XII.

From tables XI and XII , we deduce the following result which gives various possibilities of nonnegative solutions of (44).

Lemma A.1: Assume that $\mathcal{N} > 1$ and $\mu_v = \mu_1 = \mu_2$. Then, the arboviral-disease model (3)

TABLE XI
TOTAL NUMBER OF POSSIBLE REAL ROOTS OF (44) WHEN $R_0 > 1$.

Cases	B_0	B_1	B_2	B_3	B_4	Number of sign changes
	–	+	+	+	+	1
1	–	–	+	+	+	1
	–	–	–	+	+	1
	–	–	–	–	+	1
	–	+	+	–	+	3
	–	+	–	+	+	3
2	–	+	–	–	+	3
	–	–	+	–	+	3

TABLE XII
TOTAL NUMBER OF POSSIBLE REAL ROOTS OF (44) WHEN $R_0 < 1$.

Cases	B_0	B_1	B_2	B_3	B_4	Number of sign changes
1	+	+	+	+	+	0
	+	+	+	–	+	2
	+	+	–	+	+	2
	+	+	–	–	+	2
2	+	–	+	+	+	2
	+	–	–	+	+	2
	+	–	–	–	+	2
3	+	–	+	–	+	4

1. has a unique endemic equilibrium when Case 1 of Table XI is satisfied and whenever $R_0 > 1$.
2. could have more than one endemic equilibrium when Case 2 of Table XI is satisfied whenever $R_0 > 1$.
3. could have more than one endemic equilibrium when Case 2, 3 of Table XII are satisfied and whenever $R_0 < 1$.
4. has no endemic equilibrium when Case 1 of Table XII is satisfied and whenever $R_0 < 1$.

Case 3 of Lemma A.1 suggests that co-existence of the disease–free equilibrium and the endemic equilibrium for the arboviral-disease model (3) is possible, and hence the potential occurrence of the backward bifurcation phenomenon when $R_0 < 1$. Also, case 2 of Lemma A.1 suggests the possibility of a pithcfork (Forward) bifurcation when $R_0 = 1$.

b) Presence of disease–induced death in vector:: Here, we will consider $\mu_v < \mu_1 < \mu_2$ with $\mu_v \neq \mu_2$. Equation (27) becomes

$$\lambda_h^* = \frac{\beta_{hv}\mu_h\mu_v k_2k_3k_{10}(k_1+\lambda_h^*)(\mu_h+\pi\lambda_h^*)}{k_2k_3k_7(k_1+\lambda_h^*)(\mu_h+\pi\lambda_h^*)-\delta\gamma_h\Lambda_h\lambda_h^*(k_8+\pi\lambda_h^*)} \times \left(\frac{\mu_2\mu_b\theta k_4\mathcal{N}_1+\alpha\lambda_v^*}{\mu_b\theta(\mu_2k_4+k_5\lambda_v^*)}\right)\left(\frac{\lambda_v}{\mu_v+\lambda_v}\right) \tag{45}$$

with $k_{12} = \dfrac{\mu_v k_{10}}{K}$, $\mathcal{N}_1 = \left(1-\dfrac{1}{\mathcal{N}}\right)$ and

$$\lambda_v^* = \frac{\beta_{vh}\mu_h\Lambda_h k_{11}\lambda_h^*(k_8+\pi\lambda_h^*)}{k_2k_3k_7(k_1+\lambda_h^*)(\mu_h+\pi\lambda_h^*)-\delta\gamma_h\Lambda_h\lambda_h^*(k_8+\pi\lambda_h^*)} \tag{46}$$

Substituting (46) in (45) gives the following equation

$$\lambda_h^*\sum_{i=0}^{6} C_i(\lambda_h^*)^i = 0 \tag{47}$$

where $C_0 = k_1^3k_2^3k_3^3k_4k_7^3\theta\mu_2\mu_v\mu_b\mu_h^3\left(R_0^2-1\right)$ and
$C_6 = -\mu_b\pi^3\theta X\left(\mu_2k_4X+\beta_{vh}k_5k_{11}\Lambda_h\mu_h\right)$
$\times\left(\mu_vX+\beta_{vh}k_{11}\Lambda_h\mu_h\right)$,

with $X = (k_2k_3k_7-\delta\Lambda_h\gamma_h) > 0$. The others coefficients C_5, C_4, C_3, C_2, and C_1 are obtained after computations on Maxima software. We also obtain the following result which gives various possibilities of solutions of Eq. (47).

Lemma A.2: Assume that $\mathcal{N} > 1$. Then, the arboviral-disease model (3)

1. could have a unique endemic equilibrium whenever $R_0 > 1$.
2. could have more than one endemic equilibrium whenever $R_0 > 1$.
3. haven't endemic equilibrium whenever $R_0 < 1$.
4. could have one or more than one endemic equilibrium whenever $R_0 < 1$.

Case 4 of Lemma A.2 suggests that co-existence of the disease–free equilibrium and endemic equilibrium for the arboviral-disease model (3) is possible, and hence the potential occurrence of a backward bifurcation phenomenon when $R_0 < 1$. Also, case 2 of Lemma A.2 suggests the possibility of a pithcfork (Forward) bifurcation when $R_0 = 1$.

Appendix E: Computation of $a^\star$ of Theorem 4.1.

$$a^\star = \frac{1}{2}v_3\sum_{i,j=1}^{9} w_iw_j\frac{\partial^2 f_3(0,0)}{\partial x_i\partial x_j} + \frac{1}{2}v_8\sum_{i,j=1}^{9} w_iw_j\frac{\partial^2 f_8(0,0)}{\partial x_i\partial x_j}. \tag{48}$$

Let $a_3^\star = \sum_{i,j=1}^{9} w_iw_j\dfrac{\partial^2 f_3(0,0)}{\partial x_i\partial x_j}$ and $a_8^\star = \sum_{i,j=1}^{9} w_iw_j\dfrac{\partial^2 f_8(0,0)}{\partial x_i\partial x_j}$. After few computations, we obtain

$$\begin{aligned}
a_3^\star &= \frac{\beta_{hv}^*\mu_h(\epsilon\xi\Lambda_h+m\mu_h)}{k_1(\Lambda_h+m\mu_h)^2}w_1\left(\eta_vw_8+w_9\right)\\
&+\frac{\beta_{hv}^*\pi\mu_h(\epsilon\xi\Lambda_h+m\mu_h)}{k_1(\Lambda_h+m\mu_h)^2}w_2\left(\eta_vw_8+w_9\right)\\
&-\frac{\beta_{hv}^*\mu_h\Lambda_h(\mu_h+\pi\xi)}{k_1(\Lambda_h+m\mu_h)^2}w_3\left(w_8\eta_v+w_9\right)\\
&-\frac{\beta_{hv}^*\mu_h\Lambda_h(\mu_h+\pi\xi)}{k_1(\Lambda_h+m\mu_h)^2}w_4\left(w_8\eta_v+w_9\right)\\
&-\frac{\beta_{hv}^*\mu_h\Lambda_h(\mu_h+\pi\xi)}{k_1(\Lambda_h+m\mu_h)^2}w_5\left(w_8\eta_v+w_9\right)\\
&+\frac{\beta_{hv}^*\eta_v\mu_h}{k_1(\Lambda_h+m\mu_h)^2}\left[\left(\epsilon\xi\Lambda_h+m\mu_h\right)\left(w_1+\pi\,w_2\right)\right.\\
&\left.-\Lambda_h(\mu_h+\pi\xi)w_8\left(w_3+w_4+w_5\right)\right]\\
&+\frac{\beta_{hv}^*\mu_h}{k_1(\Lambda_h+m\mu_h)^2}\left[\left(\epsilon\xi\Lambda_h+m\mu_h\right)\left(w_1+\pi\,w_2\right)\right.\\
&\left.-\Lambda_h(\mu_h+\pi\xi)w_9\left(w_3+w_4+w_5\right)\right]\\
&=\frac{\beta_{hv}^*\mu_h}{k_1(\Lambda_h+m\mu_h)^2}\left\{\left(\epsilon\xi\Lambda_h+m\mu_h\right)\left(w_1+\pi\,w_2\right)\right.\\
&\left.-\Lambda_h(\mu_h+\pi\xi)\left(w_3+w_4+w_5\right)\right\}\left(w_8\eta_v+w_9\right)\\
&+\frac{\beta_{hv}^*\mu_h}{k_1(\Lambda_h+m\mu_h)^2}\left\{\left(\epsilon\xi\Lambda_h+m\mu_h\right)\left(w_1+\pi\,w_2\right)\left(\eta_v+1\right)\right.\\
&\left.-\Lambda_h(\mu_h+\pi\xi)\left(w_3+w_4+w_5\right)\left(\eta_vw_8+w_9\right)\right\}\\
&=\frac{\beta_{hv}^*\mu_h}{k_1(\Lambda_h+m\mu_h)^2}\times\\
&\left\{\left(\epsilon\xi\Lambda_h+m\mu_h\right)\left(w_1+\pi\,w_2\right)\left(w_8\eta_v+w_9+\eta_v+1\right)\right.\\
&\left.-2\Lambda_h(\mu_h+\pi\xi)\left(w_3+w_4+w_5\right)\left(w_8\eta_v+w_9\right)\right\},
\end{aligned}$$

$$
\begin{aligned}
a_8^\star &= w_3\sum_{j=1}^{9} w_j\frac{\partial^2 f_8}{\partial x_3\partial x_j}(\mathbf{x}_0,0) + w_4\sum_{j=1}^{9} w_j\frac{\partial^2 f_8}{\partial x_4\partial x_j}(\mathbf{x}_0,0)\\
&\quad + w_7\sum_{j=1}^{9} w_j\frac{\partial^2 f_8}{\partial x_5\partial x_j}(\mathbf{x}_0,0) + w_8\sum_{j=1}^{9} w_j\frac{\partial^2 f_8}{\partial x_8\partial x_j}(\mathbf{x}_0,0)\\
&\quad + w_9\sum_{j=1}^{9} w_j\frac{\partial^2 f_8}{\partial x_9\partial x_j}(\mathbf{x}_0,0)\\
&= -\frac{\beta_{vh}\mu_h^2 K\theta\left(1-\frac{1}{\mathcal{N}}\right)}{\mu_v(\Lambda_h+\mu_h m)^2}\left[\eta_h\left(w_3+\sum_{i=1}^{5} w_i\right)+w_4\right]w_3\\
&\quad - \frac{\beta_{vh}\mu_h^2 K\theta\left(1-\frac{1}{\mathcal{N}}\right)}{\mu_v(\Lambda_h+\mu_h m)^2}\left[\left(w_4+\sum_{i=1}^{5} w_i\right)+\eta_h w_3\right]w_4\\
&\quad + \frac{\beta_{vh}\mu_h}{(\Lambda_h+\mu_h m)}\left(\eta_h w_3+w_4\right)w_7\\
&= -\frac{\beta_{vh}\mu_h^2 K\theta\left(1-\frac{1}{\mathcal{N}}\right)}{\mu_v(\Lambda_h+\mu_h m)^2}\left[\left(\eta_h w_3+w_4\right)\left(w_1+w_2+w_5\right)\right.\\
&\quad \left.+2(\eta_h+1)w_3w_4+2\left(\eta_h w_3^2+w_4^2\right)\right]\\
&\quad + \frac{\beta_{vh}\mu_h}{(\Lambda_h+\mu_h m)}\left(\eta_h w_3+w_4\right)w_7
\end{aligned}
$$

Using above results, Eq. (48) becomes

$$a^\star = \phi_1 - \phi_2$$

where

$$
\begin{aligned}
\phi_1 &= \frac{1}{2}v_3\left\{\frac{\beta_{hv}^*\mu_h}{k_1(\Lambda_h+m\mu_h)^2}\left[(\epsilon\xi\Lambda_h+m\mu_h)\left(w_1+\pi\, w_2\right)\right.\right.\\
&\quad \left.\times\left(w_8\eta_v+w_9+\eta_v+1\right)\right.\\
&\quad \left.-2\Lambda_h(\mu_h+\pi\xi)\left(w_3+w_4+w_5\right)\left(w_8\eta_v+w_9\right)\right]\}\\
&\quad -\frac{1}{2}v_8\frac{\beta_{vh}\mu_h^2 K\theta}{\mu_v(\Lambda_h+\mu_h m)^2}\left(1-\frac{1}{\mathcal{N}}\right)w_5\left(\eta_h w_3+w_4\right)\\
&\quad +\frac{1}{2}v_8\frac{\beta_{vh}\mu_h}{(\Lambda_h+\mu_h m)}\left(\eta_h w_3+w_4\right)w_7\\
&\quad -\frac{1}{2}v_8\frac{\beta_{vh}\mu_h^2 K\theta\left(1-\frac{1}{\mathcal{N}}\right)}{\mu_v(\Lambda_h+\mu_h m)^2}\left[2(\eta_h+1)w_3w_4\right.\\
&\quad \left.+2\left(\eta_h w_3^2+w_4^2\right)\right] < 0
\end{aligned}
$$

and

$$
\begin{aligned}
\phi_2 &= \frac{1}{2}v_8\frac{\beta_{vh}\mu_h^2 K\theta}{\mu_v(\Lambda_h+\mu_h m)^2}\left(1-\frac{1}{\mathcal{N}}\right)\\
&\quad \times\left[\left(\eta_h w_3+w_4\right)\left(w_1+w_2\right)\right] < 0
\end{aligned}
$$

Appendix F: Proof of Lemma 7.2

The Kamgang-Sallet approach used for (22) ensures that the trivial equilibrium($TE := P_0$) and the disease–free equilibrium ($DFE := P_1$) are the fixed point of (22). Indeed, rewriting (22) gives

$$
\left\{\begin{array}{ll}
S_h^{k+1} &= \dfrac{\phi(h)\Lambda_h+(1-\phi(h)k_1)S_h^k}{1+\phi(h)\lambda_h^k}\\
V_h^{k+1} &= \dfrac{\phi(h)\xi S_h^k+(1-\phi(h)\mu_h)V_h^k}{1+\phi(h)\pi\lambda_h^k}\\
E_h^{k+1} &= (1-\phi(h)k_2)E_h^k+\phi(h)\lambda_h^k\\
&\quad\times(S_h^{k+1}+\pi V_h^{k+1})\\
I_h^{k+1} &= \phi(h)\gamma_h E_h^k+(1-\phi(h)k_3)I_h^k\\
R_h^{k+1} &= \phi(h)\sigma I_h^k+(1-\phi(h)\mu_h)R_h^k\\
A_v^{k+1} &= \left[1-\phi(h)\left(k_6+\mu_b\dfrac{S_v^k+E_v^k+I_v^k}{K}\right)\right]A_v^k\\
&\quad+\phi(h)\mu_b(S_v^k+E_v^k+I_v^k)\\
S_v^{k+1} &= \dfrac{\phi(h)\theta A_v^k+(1-\phi(h)\mu_v)S_v^k}{1+\phi(h)\lambda_v^k}\\
E_v^{k+1} &= (1-\phi(h)k_4)E_v^k+\phi(h)\lambda_v^k S_v^{k+1}\\
I_v^{k+1} &= \phi(h)\gamma_v E_v^k+(1-\phi(h)\mu_2)I_v^k
\end{array}\right. \tag{49}
$$

If $X^* = (S_h, V_h^*, E_h^*, I_h^*, R_h^*, A_v^*, S_v^*, E_v^*, I_v^*)^T$ is an equilibrium of the discrete system (49), then we have after few simplifications

$$
\left\{\begin{array}{ll}
\Lambda_h-\lambda_h^*S_h^*-k_1S_h^* &= 0\\
\xi S_h^*-\pi\lambda_h^*V_h^*-\mu_h V_h^* &= 0\\
\lambda_h^*(S_h^*+\pi V_h^*)-k_2E_h^* &= 0\\
\gamma_h E_h^*-k_3I_h^* &= 0\\
\sigma I_h^*-\mu_h R_h^* &= 0\\
\mu_b(S_v^*+E_v^*+I_v^*)\left(1-\dfrac{A_v^*}{K}\right)-k_6A_v^* &= 0\\
\theta A_v^*-\lambda_v^*S_v^*+\mu_v S_v^* &= 0\\
k_4E_v^*-\lambda_v^*S_v^* &= 0\\
\gamma_v E_v^*-\mu_2 I_v^* &= 0
\end{array}\right. \tag{50}
$$

which is equivalent to

$$
\left\{\begin{array}{ll}
\mathcal{A}_1(X^*)(X_S^*-X_{DFE})+\mathcal{A}_{12}(X^*)X_I^* &= 0\\
\mathcal{A}_2(X^*)X_I^* &= 0
\end{array}\right. \tag{51}
$$

where $\mathcal{A}_1$, $\mathcal{A}_{12}$ and $\mathcal{A}_2$ are given at Equation (11).

Appendix G: Proof of Lemma 7.3

The Jacobian matrix associated with the right-hand side of the numerical scheme (22) at the

tivial equilibrium $TE := P_0$ is given by $\mathcal{J}_{TE} = (\mathcal{J}_{ij})_{1\leq i,j\leq 9}$ with

$$J_{1,1} = 1 - k_1\phi(h); J_{1,8} = -\frac{\phi(h)\beta_{hv}\eta_v\Lambda_h\mu_h}{k_1(\Lambda_h+\mu_h m)};$$
$$J_{1,9} = -\frac{\phi(h)\beta_{hv}\Lambda_h\mu_h}{k_1(\Lambda_h+\mu_h m)}; J_{2,1} = \phi(h)\xi;$$
$$J_{2,2} = 1 - \mu_h\phi(h);$$
$$J_{2,8} = -\frac{\phi(h)\pi\beta_{hv}\eta_v\xi\Lambda_h}{k_1(\Lambda_h+\mu_h m)},$$
$$J_{2,9} = -\frac{\phi(h)\pi\beta_{hv}\xi\Lambda_h}{k_1(\Lambda_h+\mu_h m)},$$
$$J_{3,3} = 1 - k_2\phi(h);$$
$$J_{3,8} = \frac{\phi(h)\beta_{hv}\eta_v\Lambda_h(\mu_h+\pi\xi)}{k_1(\Lambda_h+\mu_h m)};$$
$$J_{3,9} = \frac{\phi(h)\beta_{hv}\Lambda_h(\mu_h+\pi\xi)}{k_1(\Lambda_h+\mu_h m)}; J_{4,3} = \phi(h)\gamma_h,$$
$$J_{4,4} = 1 - k_3\phi(h); \quad J_{5,4} = \phi(h)\sigma;$$
$$J_{5,5} = 1 - \mu_h\phi(h); \quad J_{6,6} = 1 - \phi(h)k_6;$$
$$J_{6,7} = J_{6,8} = J_{6,9} = \phi(h)\mu_b;$$
$$J_{7,6} = \phi(h)\theta, \quad J_{7,7} = 1 - \phi(h)\mu_v,$$
$$J_{8,8} = 1 - \phi(h)k_4; \quad J_{9,8} = \phi(h)\gamma_v;$$
$$J_{9,9} = 1 - \mu_2\phi(h)$$

The eigenvalues of $\mathcal{J}_{TE}$ are given by $\lambda_1 = \lambda_2 = 1 - \mu_h\phi(h)$, $\lambda_3 = 1 - k_1\phi(h)$, $\lambda_4 = 1 - k_2\phi(h)$, $\lambda_5 = 1 - k_3\phi(h)$, and λ_6, λ_7, λ_8, λ_9 are eigenvalues of the submatrix

$$\bar{\mathcal{J}} = \begin{pmatrix} J_{6,6} & \phi(h)\mu_b & \phi(h)\mu_b & \phi(h)\mu_b \\ J_{7,6} & J_{7,7} & 0 & 0 \\ 0 & 0 & J_{8,8} & 0 \\ 0 & 0 & J_{9,8} & J_{9,9} \end{pmatrix}$$

Since $\phi(h) > 0$, it is clear that $|\lambda_i| < 1$, for $i = 1, 2, \ldots, 5$. We need also to show that the characteristic polynomial associated with $\bar{\mathcal{J}}$ is Schur polynomials, i.e. polynomials such that all roots λ_i verify $|\lambda_i| < 1$.

The characteristic polynomial associated with $\bar{\mathcal{J}}$ is given by
$P(\lambda) = (\lambda + \mu_2\phi(h) - 1)(\lambda + k_4\phi(h) - 1) H(\lambda)$
where

$$H(\lambda) = \lambda^2 + (\phi(h)(\mu_v + k_6) - 2)\lambda + 1 + \phi(h)^2(k_6\mu_v - \mu_b\theta) - \phi(h)(\mu_v + k_6)$$

The roots of $P(\lambda)$ are $\lambda_6 = 1 - \mu_2\phi(h)$, $\lambda_7 = 1 - k_4\phi(h)$ and the others roots are the roots of $H(\lambda)$. Note that $|\lambda_6| < 1$ and $|\lambda_7| < 1$. Now, we need to show that $H(\lambda)$ is a Schur polynomial. To this aim, let $q_1 = (\phi(h)(\mu_v + k_6) - 2)$
and $q_2 = 1 + \phi(h)^2(k_6\mu_v - \mu_b\theta) - \phi(h)(\mu_v + k_6)$. Using Lemma 11 in [29], we just show that the following conditions hold:

$$1 + q_1 + q_2 > 0, \qquad 1 - q_1 + q_2 > 0, \quad 1 - q_2 > 0 \tag{52}$$

We compute $1 + q_1 + q_2 = \phi(h)^2 k_6\mu_v(1 - \mathcal{N})$,
$1 - q_1 + q_2 = 2\left[(1 - \phi(h)\mu_v) + (1 - \phi(h)k_6)\right] + \phi(h)^2 k_6\mu_v(1 - \mathcal{N})$ and
$1 - q_2 = \phi(h)\left[\mu_v + k_6(1 - \phi(h)\mu_v) + \phi(h)\mu_b\theta\right]$

If $\phi(h)$ has choosen as equation (25), then conditions (52) hold whenever $\mathcal{N} \leq 1$. Thus, $H(\lambda)$ is a Schur polynomial. This ends the proof.

REFERENCES

[1] Ahmed Abdelrazec, Suzanne Lenhart, Huaiping Zhu, *Transmission dynamics of West Nile virus in mosquitoes and corvids and non-corvids*, J. Math. Biol. (2014) 68:1553–1582. DOI10.1007/s00285-013-0677-3

[2] Dipo Aldila, Thomas Gtz, Edy Soewono, An optimal control problem arising from a dengue disease transmission model, Mathematical Biosciences 242 (2013) 9–16.

[3] R. Anguelov, J. M. S. Lubuma, M. Shillor, *Topological dynamic consistency of nonstandard finite difference schemes for dynamical systems*, J. Difference Eq. Appl., 17, 1769–1791 (2011)

[4] R. Anguelov, Y. Dumont, J. M. S. Lubuma, *On nonstandard finite difference schemes in biosciences*, Proceeding of the fourth international conference on application of mathematics in technical and natural sciences. American Institute of Physics conference, Proceedings AIP, 1487, 212–223 (2012)

[5] R. Anguelov, Y. Dumont, J.M.-S. Lubuma, and M. Shillor, *Dynamically consistent nonstandard finite difference schemes for epidemiological Models*. Journal of Computational and Applied Mathematics, 255, pp.161-182, 2014.

[6] Arino J., McCluskey C.C., van den Driessche P., Global results for an epidemic model with vaccination that exhibits backward bifurcation, SIAM Journal on Applied Mathematics 64 (2003) 260–276.

[7] Bayer 360° Vector Control. Available at http://www.vectorcontrol.bayer.com/bayer/cropscience/bes_vectorcontrol.nsf/id/EN_mosquitoes (Retrieved January 2014)

[8] A. Berman, R.J. Plemmons, *Nonnegative matrices in the mathematical sciences*, SIAM., 1994.

[9] N. P. Bhatia, G. P. Szego, *Stability Theory of Dynamical Systems*, Springer-Verlag, 1970

[10] Jr J.E. Blaney, N.S. Sathe, C.T. Hanson, C.Y. Firestone, B.R. Murphy, S.S. Whitehead, *Vaccine candidates for dengue virus type 1 (Den 1) generated by replacement of the structural genes of rDen 4 and rDen4D30 with those of Den 1*, Virology Journal 4 (23) (2007) 1–11.

[11] Jr J.E. Blaney, J.M. Matro, B.R. Murphy, S.S. Whitehead, *Recombinant, live-attenuated tetravalent dengue virus vaccine formulations induce a balanced, broad, and protective neutralizing anitibody response against each of the four serotypes in rhesus monkeys*, Journal of Virology 79 (9) (2005) 5516–5528.

[12] S. Blower, H. Dowlatabladi, *Sensitivity and uncertainty analysis of complex models of disease transmission: an HIV model, as an example*. Int. Stat. Rev., 62, 229–243 (1994)

[13] Boloye Gomero, *Latin Hypercube Sampling and Partial Rank Correlation Coefficient Analysis Applied to an Optimal Control Problem*, Master Thesis, University of Tennessee, Knoxville, 2012.

[14] Brauer F., Backward bifurcations in simple vaccination models, J. Math. Anal. Appl., 298, 418-431 (2004)

[15] Buonomo B., D. Lacitignola, A note on the direction of the transcritical bifurcation in epidemic models. Nonlinear Analysis: Modelling and Control, 2011, Vol. 16, No. 1, 30–46.

[16] Buonomo B., On the backward bifurcation of a vaccination model with nonlinear incidence. Nonlin. Anal. Mod. Control, 20, 38–55 (2015).

[17] J. R. Cannon, D. J. Galiffa, *An epidemiology model suggested by yellow fever*, Math. Methods Appl. Sci., 35, 196–206 (2012)

[18] V. Capasso, *Mathematical Structures of Epidemics Systems. Lecture Notes in Biomathematics*, 97. Springer-Verlag, Berlin, 2008

[19] C. Castillo–Chavez, B. Song, *Dynamical models of tuberculosis and their applications*, Math. Biosci. Eng, 1, 361–404 (2004)

[20] A. Chippaux, *Généralités sur arbovirus et arboviroses, overview of arbovirus and arbovirosis*, Med. Maladies Infect., 33, 377–384 (2003)

[21] N. Chitnis, D. Hardy, T. Smith, *A Periodically–Forced Mathematical Model for the Seasonal Dynamics of Malaria in Mosquitoes*. Bull. Math. Biol. 74, 1098–1124 (2012)

[22] N. Chitnis, J. M. Hyman, J. M. Cushing, *Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model*, Bull. Math. Biol., 70, 1272–1296 (2008)

[23] F.A.B. Coutinho, M.N. Burattini, L.F. Lopez, E. Massad, *Threshold conditions for a non-autonomous epidemic system describing the population dynamics of dengue*, Bulletin of Mathematical Biology 68 (2006) 2263–2282.

[24] G. Cruz-Pacheco, L. Esteva, C. Vargas, *Seasonality and outbreaks in West Nile Virus infection*, Bull. Math. Biol., 71, 1378–1393 (2009)

[25] Cushing J. M. and Yicang Z., The net reproductive value and stability in matrix population models, Nat. Resour. Model., 8 (1994), pp. 297–333.

[26] O. Diekmann, J. A. P. Heesterbeek, *Mathematical Epidemiology of Infectious Diseases. Model building, analysis and interpretation*. John Wiley & Sons, Chichester, 2000

[27] K. Dietz, *Transmission and control of arbovirus diseases*, Epidemiology (ed. D. Ludwig, K. L. Cooke), pp. 104–121, SIAM, Philadelphia, 1975

[28] M. Dubrulle, L. Mousson, S. Moutailler, M. Vazeille and A.-B. Failloux, *Chikungunya virus and aedes mosquitoes: Saliva is infectious as soon as two days after oral infection*, PLoS One, 4 (2009).

[29] Y. Dumont, F. Chiroleu, C. Domerg, *On a temporal model for the Chikungunya disease: Modeling, theory and numerics*, Mathematical Biosciences 213 (2008) 80–91.

[30] Y. Dumont, F. Chiroleu, *Vector control for the chikungunya disease*, Math. Biosci. Eng., 7, 313–345 (2010)

[31] J. Dushoff, W. Huang, C. Castillo–Chavez, *Backward bifurcations and catastrophe in simple models of fatal diseases*, J. Math. Biol., 36, 227–248 (1998)

[32] M. Dubrulle, L. Mousson, S. Moutailler, M. Vazeille, A.-B. Failloux, *Chikungunya virus and aedes mosquitoes: Saliva is infectious as soon as two days after oral infection*, PLoS One, 4 (2009).

[33] K.H. Eckels, R. Putnak, *Formalin-inactivated whole virus and recombinant subunit flavivirus vaccine*s, Advances in Virus Research 61 (2003) 395–418.

[34] Y. Eshita, T. Takasaki, I. Takashima, N. Komalamisra, H. Ushijima and I. Kurane, *Vector competence of Japanese mosquitoes for dengue and West Nile viruses*, Pesticide Chemistry (2007) doi:10.1002/9783527611249.ch23.

[35] L. Esteva, C. Vargas, *Analysis of a dengue disease transmission model*, Math. Biosci., 150, 131–151 (1998)

[36] L. Esteva, C. Vargas, *A model for dengue disease with variable human population*, J. Math. Biol., 38, 220–240 (1999)

[37] F. Forouzannia, A.B. Gumel, *Mathematical Analysis of an Age-structured Model for Malaria Transmission Dynamics*, Mathematical Biosciences (2013), doi:http://dx.doi.org/10.1016/j.mbs.2013.10.011

[38] Z. Feng, V. Velasco–Hernandez, *Competitive exclusion in a vector–host model for the dengue fever*, J. Math. Biol., 35, 523–544 (1997)

[39] Figaro, Un vaccin contre la dengue disponible dès la mi-2015. http://www.lefigaro.fr/societes/2014/11/04/20005-20141104ARTFIG00301-un-vaccin-contre-la-dengue-disponible-des-la-mi-2015.php (Accessed April 2015)

[40] S.M. Garba, A.B. Gumel, M.R. Abu Bakar, *Backward bifurcations in dengue transmission dynamics*, Math. Biosci., 215, 11–25 (2008)

[41] B. S. Goh, *Global stability in a class of prey-predator models*. Bull. Math. Biol. 40, 525-533 (1978)

[42] D. J. Gubler, *Human arbovirus infections worldwide*, Ann. N. Y. Acad. Sci., 951, 13–24 (2001)

[43] J. Guckenheimer, P. Holmes, *Nonlinear Oscillations, Dynamical Systems and Bifurcations of Vector Fields*, Springer-Verlag, Berlin, 1983.

[44] L. Guillaumot, *Les moustiques et la dengue (in French)*. Institut Pasteur de Nouvelle–Caledonie, 2005

[45] J. K. Hale, *Ordinary Differential Equations*. John Wiley and Sons, New York. 1969

[46] Institut Pasteur, Chikungunya. http://www.pasteur.fr/fr/institut-pasteur/presse/fiches-info/chikungunya#Traitement (Accessed August 2014)

[47] J.A. Jacquez, C.P. Simon,*Qualitative theory of compartmental systems*. SIAM Rev. 35 (1993), 43–79.

[48] J. C. Kamgang, G. Sallet, *Computation of threshold conditions for epidemiological models and global stability of the disease-free equilibrium (DFE)*, Mathematical Biosciences 213 (2008) 1–12.

[49] N. Karabatsos, *International Catalogue of Arboviruses, including certain other viruses of vertebrates*. American Society of Tropical Medicine and Hygiene. San Antonio, TX. 1985, 2001 update

[50] P. Koraka, S. Benton, G. van Amerongen, K.J. Stitelaar, A.D.M.E. Osterhaus, *Efficacy of a live attenuated tetravalent candidate dengue vaccine in naive and previously infected cynomolgus macaques*, Vaccine 25 (2007) 5409–5416.

[51] J. P. LaSalle, *Stability theory for ordinary differential equations*, J. Differ. Equ., 57–65 (1968)

[52] J. P. LaSalle, *The stability of dynamical systems*, Society for Industrial and Applied Mathematics, Philadelphia, Pa., 1976.

[53] Le Figaro, *Chikungunya: Des vaccins bientôt testés chez l'homme*, http://www.lefigaro.fr/sciences (Accessed August 2014)

[54] Le Monde, *Test prometteur pour un nouveau vaccin contre le chikungunya*, http://www.lemonde.fr/sante/article (Accessed August 2014)

[55] Lee-Jah Chang et al., *Safety and tolerability of chikungunya virus-like particle vaccine in healthy adults: a phase 1 dose–escalation trial*. http://dx.doi.org/10.1016/S0140-6736(14)61185-5.

[56] N. A. Maidana, H. M. Yang, *Dynamic of West Nile Virus transmission considering several coexisting avian populations*, Math. Comput. Modelling, 53, 1247–1260 (2011)

[57] MATLAB©. *Matlab release 12*. The mathworks Inc., Natich, MA, 2000.

[58] Michel Gosse, *Faq Maxima*, Version 0.93 du 13 juillet 2010.

[59] R. E. Mickens, *Nonstandard Finite Difference Models of Differential Equations*. World Scientific, Singapore, 1994

[60] D. Moulay, M. A. Aziz–Alaoui, M. Cadivel, *The Chikungunya disease: Modeling, vector and transmission global dynamics*, Math. Biosci., 229,50–63 (2011)

[61] Moulay D., Aziz–Alaoui M. A., Hee-Dae Kwon, Optimal control of Chikungunya disease: larvae reduction,treatment and prevention, Mathemtical Biosciences and Engineering, volume 9, Number 2, April 2012.

[62] S. Naowarat, W. Tawarat, I. Ming Tang, *Control of the transmission of chikungunya fever epidemic through the use of adulticide*, Am. J. Appl. Sci., 8, 558–565 (2011)

[63] S. Naowarat, P. Thongjaem, I. Ming Tang, *Effect of mosquito repellent on the transmission model of chikungunya fever*, Am. J. Appl. Sci., 9, 563–569 (2012)

[64] P. Poletti, G. Messeri, M. Ajelli, R. Vallorani, C. Rizzo, S. Merler, *Transmission potential of chikungunya virus and control measures: the case of Italy*, PLoS One, 6, e18860 (2011)

[65] Richard Taylor. *Interpretation of the correlation coefficient: A basic review*, Journal of Diagnostic Medical Sonography, 6(1):35–39, 1990.

[66] R Development Core Team: a language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, http://www.r-395project.org/foundation

[67] H.S. Rodrigues, M.T.T. Monteiro, D.F.M. Torres, A. Zinober, *Dengue disease, basic reproduction number and control*, Int. J. Comput. Math. 89 (3) (2012) 334.

[68] H. S. Rodrigues, M. Teresa T. Monteiro, Delfim F.M. Torres, *Vaccination models and optimal control strategies to dengue*, Mathematical Biosciences 247 (2014) 1–12.

[69] H.S. Rodrigues, M.T.T. Monteiro, D.F.M. Torres, *Insecticide control in a dengue epidemics model*, in: T.E. Simos, et al. (Eds.), Numerical analysis and applied mathematics. International conference on numerical analysis and applied mathematics, Rhodes, Greece. American Institute of Physics Conf. Proc., no. 1281 in American Institute of Physics Conf. Proc., 2010, pp. 979–982.

[70] M. Safan, M. Kretzschmar, K. P. Hadeler, *Vaccination based control of infections in SIRS models with reinfection: special reference to pertussis*, J. Math. Biol., 67, 1083–1110 (2013)

[71] M. Sanchez, S. Blower, *Uncertainty and sensitivity analysis of the basic reproductive rate*. American Journal of Epidemiology, 145: 1127 - 1137 (1997)

[72] SANOFI PASTEUR, *Dengue vaccine, a priority for global health*, (2013)

[73] J.F. Saluzzo, *Empirically derived live attenuated vaccines against dengue and Japanese encephalitis*, Advances in Virus Research 61 (2003), 419–443.

[74] A. J. Saul, P. M. Graves, B. H. Kay, *A cyclical feeding model for pathogen transmission and its application to determine vectorial capacity from vector infection*. J. Appl. Ecology, 27, 123–133 (1990)

[75] O. Sharomi, C.N. Podder, A.B. Gumel, E.H. Elbasha, J. Watmough, *Role of incidence function in vaccine-induced backward bifurcation in some HIV models*, Mathematical Biosciences 210 (2007) 436–463.

[76] SCILAB. Open source software for numerical computation. http://www.scilab.org

[77] Z. Shuai, P. van den Driessche, *Global dynamics of a*

disease model including latency with distributed delays. Can. Appl. Math. Q., 19, 235–253 (2012).

[78] M. Stein, *Large Sample Properties of Simulations Using Latin Hypercube Sampling*. Technometrics, 29, 143–151 (1987)

[79] A.K. Supriatna, E. Soewono, S.A. van Gils, *A two-age-classes dengue transmission model*, Mathematical Biosciences 216 (2008) 114–121.

[80] J. J. Tewa, J. L. Dimi, S. Bowong, *Lyapunov functions for a dengue disease transmission model*, Chaos Solit. Fract., 39, 936–941 (2009)

[81] Valaire Yatat, Yves Dumont, Jean Jules Tewa, Pierre Courteron, Samuel Bowong, *Mathematical Analysis of a Size Tree-Grass Competition Model for savanna Ecosystems*, BIOMATH 3 (2014),1404214, http://dx.doi.org/10.11145/j.biomath.2014.04.212

[82] P. van den Driessche,J. Watmough, *Reproduction numbers and the sub-threshold endemic equilibria for compartmental models of disease transmission*, Math. Biosci., 180, 29–48 (2002)

[83] C. Vargas, L. Esteva, G. Cruz–Pacheco, *Mathematical modelling of arbovirus diseases*, 7th International Conference on Electrical Engineering, Computing Science and Automatic Control, CCE 2010

[84] World Health Organization. *Dengue and severe dengue*. Fact sheet n.117. Updated September 2013. Available at www.who.int/mediacentre/factsheets/fs117/en (Retrieved January 2014)

[85] World Health Organization, *Immunological correlates of protection induced by dengue vaccines*, Vaccine. 25 (2007) 4130–4139.

[86] World Health Organization, *Dengue and dengue haemorhagic fever*, factsheet No.117, 2009.

[87] A. Wilder–Smith, W. Foo, A. Earnest, S. Sremulanathan, N.I. Paton, *Seroepidemiology of dengue in the adult population of Singapore*, Tropical Medicine and International Health 9 (2) (2004) 305–308.

[88] L. Wu, B. Song, W. Du, J. Lou, *Mathematical modelling and control of echinococcus in Qinghai province*, China, Math. Biosci. Eng., 10, 425–444 (2013)

[89] wxMaxima 11.08.0© 2004–2011 Andrej Vodopivec, http://andrejv.github.com/wxmaxima/

[90] A. Yebakima et al., *Genetic heterogeneity of the dengue vector Aedes aegypti in Martinique*, Tropical Medicine and International Health 9 (5) (2004) 582–587.